

# **Bacteria TMDL for Deep Run Stafford and Fauquier County, Virginia**

**Submitted by:**

**Virginia Department of Environmental Quality**

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## **List of Acronyms**

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AVMA	American Veterinary Medical Association
BASINS	Better Assessment Science Integrating Point and Nonpoint Sources
BMPs	Best Management Practices
BST	Bacterial Source Tracking
HSPF	Hydrologic Simulation Program – Fortran
LA	Load Allocation
MOS	Margin of Safety
MPN	Most Probable Number
MRLC	Multi-Resolution Land Characterization
MS4	Phase II Municipal Separate Storm Sewer System
NCDC	National Climatic Data Center
NLCD	National Land Cover Data
NRCS	Natural Resources Conservation Service
NWS	National Weather Service
SCS	Soil Conservation Service
SERCC	Southeast Regional Climate Center
TAC	Technical Advisory Committee
TMDL	Total Maximum Daily Load
UAA	Use Attainability Analysis
USEPA	U.S. Environmental Protection Agency
USGS	U.S. Geological Survey
VADCR	Virginia Department of Conservation and Recreation
VADEQ	Virginia Department of Environmental Quality
VADGIF	Virginia Department of Game and Inland Fisheries
VASS	Virginia Agriculture Statistics Service
VCE	Virginia Cooperative Extension
VDACS	Virginia Department of Agricultural and Consumer Services
VDH	Virginia Department of Health
VPDES	Virginia Pollutant Discharge Elimination System
VWCB	Virginia Water Control Board
WLA	Wasteload Allocation
WQMP	Water Quality Management Plan

# Executive Summary

## Background

Deep Run is a tributary of the Rappahannock River, which empties into the Chesapeake Bay. The impaired portion of Deep Run, beginning at the confluence with Green Branch just downstream of the Route 752 bridge and continuing downstream approximately 4.83 miles to the confluence with the Rappahannock River is listed as impaired by fecal coliform bacteria on Virginia's 2002 list (VADEQ, 2003b).

The Deep Run watershed (Water body ID VAN-E10R) is located in Stafford County, Virginia and Fauquier County, Virginia. The southern portion of the main stem of Deep Run runs along border between the two counties. The watershed comprises 17,283 acres and is mainly forested (about 78%). The majority of the remaining 22% of the watershed area is divided among agricultural uses. Pasture/hay and cropland land uses comprise 20 and 1.3% of the watershed area, respectively.

VADEQ personnel monitored pollutant concentrations at the Deep Run watershed outlet (Station ID No. 3-DPR001.70). Of the 16 water quality samples collected from July 1992 through June 1997 (the 1998 Section 303(d) 5-year listing period) near the outlet of the watershed, 44% of the samples exceeded the instantaneous standard of 1,000 cfu/100 mL. Consequently, this segment of Deep Run was determined as not supporting the Clean Water Act's Swimming Use Support Goal for the 1998 Section 305(b) report and was included in the 1998 Section 303(d) list (VADEQ, 2003a). The Deep Run segment was further listed on the 2002 Section 303(d) list (VADEQ, 2003b).

In order to remedy the water quality impairment pertaining to fecal coliform, a Total Maximum Daily Load (TMDL) has been developed, taking into account all sources of bacteria and a margin of safety (MOS). The TMDL was developed for the new water quality standard for bacteria, which states that the calendar-month geometric mean concentration of *E. coli* shall not exceed 126 cfu/100 mL, and that no single sample can exceed a concentration of 235 cfu/100mL. The glossary lists terms used in the development of this TMDL.

## Sources of Fecal Coliform

There are no point sources permitted to discharge fecal coliform in the Deep Run watershed, therefore the fecal coliform load originates from nonpoint sources. Nonpoint sources of fecal coliform are primarily agricultural (i.e., land-applied animal waste, manure deposited directly on pastures by livestock, and a significant fecal coliform load due to cattle directly depositing manure in streams) with a significant load applied to residential and forest land use categories. Non-agricultural anthropogenic nonpoint sources of fecal coliform loadings include straight pipes, failing septic systems, and pet waste. Wildlife contributes to fecal coliform loadings on all land uses, according to the acceptable habitat range for each species. The amounts of fecal coliform produced in different locations (e.g., confinement, pasture, forest) were estimated on a monthly basis to account for seasonal variability in wildlife habitat and livestock production and practices. Livestock management and production factors, such as the

fraction of time cattle spend in confinement or in streams and the amount of manure storage and spreading schedules were considered on a monthly basis.

## **Modeling**

The Hydrologic Simulation Program – Fortran (HSPF) was used to simulate the fate and transport of fecal coliform bacteria in the Deep Run watershed. To identify localized sources of fecal coliform, the Deep Run watershed was divided into eight subwatersheds. These subdivisions were based primarily on homogeneity of land use.

Observed stream flow values were not available for Deep Run, therefore a “paired watershed” approach was used for hydrologic calibration and validation. The approach assumes that the paired watershed and Deep Run watershed have similar hydrologic responses based on physical, geologic, and hydrologic characteristics. The Battle Run watershed was chosen as the paired watershed based on comparable size, land use distribution, slope, prominent soil hydrologic group, and geology.

Hydrology calibration and validation was performed based on data describing the Battle Run watershed. Observed daily average flows from U.S. Geologic Survey (USGS) station at Battle Run near Laurel Mills, VA (#01662800) was used to calibrate the hydrology component of HSPF for the period March 1, 1981 to June 15, 1985 (USGS, 2003). The calibration period covered a wide range of hydrologic conditions, including low- and high-flow conditions, as well as seasonal variations. The calibrated HSPF data set was validated on a separate period of record from January 1, 1990 to June 30, 1993. After calibration and validation completion, the dataset for the Battle Run model was transferred to the Deep Run model. The model was updated with parameters specifically describing Deep Run watershed characteristics including land use, slope, infiltration rate, and F-Tables. The calibrated HSPF model adequately simulated the hydrology of the Deep Run watershed.

The water quality component of the HSPF model was calibrated using fecal coliform data collected at four VADEQ monitoring stations between January 1998 and December 2002 in the Deep Run watershed. The model was validated for period January 1992 to December 1997 using fecal coliform data collected at one VADEQ station in the Deep Run watershed. Inputs to the model included fecal coliform loadings on land and in the stream along with simulated flow data. A comparison of simulated and observed fecal coliform loadings in the stream indicated that the model adequately simulated the fate and transport of fecal coliform in the watershed.

## **Margin of Safety**

A margin of safety (MOS) was included to account for any uncertainty in the TMDL development process. There are several different ways that the MOS could be incorporated into the TMDL (USEPA, 1991). For the Deep Run TMDL, the MOS was implicitly incorporated into the TMDL by conservatively estimating several factors affecting bacteria loadings, such as animal numbers, production rates, and contributions to streams.

## Existing Conditions

Based on amounts of fecal coliform produced in different locations, daily fecal coliform loadings to different land use categories were calculated for each sub-watershed for input into the model. Fecal coliform content of stored waste was adjusted to account for die-off during storage prior to land application. Similarly, fecal coliform die-off on land was taken into account, as was the reduction in fecal coliform available for surface wash-off due to incorporation following waste application on cropland. Straight pipes produced a direct fecal coliform load to the stream. Direct seasonal fecal coliform loadings to streams by cattle were calculated for pastures adjacent to streams. Fecal coliform loadings to streams and land by wildlife were estimated for several species. Fecal coliform loadings to land from failing septic systems were estimated based on number and age of houses. Fecal coliform contribution from pet waste was also considered. Contributions from these various sources were represented in HSPF to establish existing conditions for a representative hydrologic period (January 1993 through December 1997).

## TMDL Allocation Scenarios

After calibrating to the existing water quality conditions, different scenarios were evaluated to identify implementable scenarios that meet both the calendar-month geometric mean *E. coli* criterion (126 cfu/100 mL) and the single sample maximum *E. coli* criterion (235 cfu/100 mL) with zero violations. Scenarios were evaluated to predict the effects of different combinations of source reductions on final in-stream water quality.

The selected TMDL allocation that meets both the calendar-month geometric mean and single sample water quality goals requires a 100% reduction in straight pipes, 99% reduction in direct deposits of livestock manure to streams, 99% reduction in nonpoint source loadings to residential and pasture land uses, 88% reduction in nonpoint source loadings to cropland, 0% reduction in direct deposits by wildlife to streams, and 0% reduction in nonpoint source loadings to forest land use. Using equation [E.1], summary of the Deep Run bacteria TMDL for the selected allocation scenario is shown in Table E.1.

$$\text{TMDL} = \text{WLA} + \text{LA} + \text{MOS} \quad [\text{E.1}]$$

where: WLA = wasteload allocation (point source contributions);  
LA = load allocation (nonpoint source contributions); and  
MOS = margin of safety (implicit).

**Table E.1. Average annual *E. coli* bacteria loads (cfu/yr) modeled after TMDL allocation in Deep Run watershed.**

Pollutant	WLA (cfu/yr)	LA (cfu/yr)	MOS	TMDL (cfu/yr)
<i>E. coli</i>	0.0	3.19E+13	N/A	3.19E+13

N/A – not applicable because MOS was implicit.

## **Stage 1 Implementation**

The TMDL allocation scenario developed for the Deep Run impairment forms a basis for developing implementation strategies. Staged implementation is a key component to restoring water quality in Deep Run. An alternative scenario was evaluated to establish goals for the first stage of the implementation of the TMDL. The implementation of such a transitional scenario, or Stage 1 implementation, will allow for an evaluation of the effectiveness of management practices and accuracy of model assumptions through continued data collection. The Stage 1 implementation scenario providing an instantaneous standard violation rate below 10% and 0% reduction in loads from wildlife requires a 100% reduction in straight pipes, 99% reduction in livestock direct deposition, and 88% reduction in nonpoint source loadings to residential, cropland, and pasture land uses.

## **Public Participation**

During development of the Deep Run TMDL, public participation was encouraged through three public meetings. The first public meeting was held at the Mary Walter Elementary School in Bealeton on April 2, 2003 to discuss the need for a TMDL and the process for TMDL development. The second public meeting was also held at the Mary Walter Elementary School on September 17, 2003 to discuss the draft watershed source assessment, and to review the approach for TMDL development. The third and final public meeting was again held at the Mary Walter Elementary School on March 10, 2004 to discuss the source allocations and reductions required to meet the TMDL. One comment was received during the 30-day comment period following the third public meeting.

In addition to keeping the public apprised of progress in the development of the Deep Run TMDL, a Technical Advisory Committee (TAC) was also established to help advise the TMDL developers. TAC meetings were held on February 21, 2003, August 21, 2003, and February 26, 2004. The TAC membership included representatives from the following agencies and organizations: Virginia Department of Environmental Quality, Virginia Department of Conservation and Recreation, Virginia Department of Game and Inland Fisheries, Culpeper County Planning, Fauquier County Planning, Stafford County Planning, Culpeper SWCD, John Marshall SWCD, Tri-City/County SWCD, VA Cooperative Extension, Natural Resources Conservation Service, and Friends of the Rappahannock.

The meetings were used as a forum to facilitate understanding of, and involvement in, the TMDL process. Data and assumptions used in the TMDL development were reviewed along with stakeholder concerns about the implications of the TMDL. Feedback from these meetings was used in the TMDL development and improved confidence in the allocation.

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# Chapter 1. Introduction

## 1.1 Background

### 1.1.1 TMDL Definition and Regulatory Information

Section 303(d) of the Federal Clean Water Act and the U.S. Environmental Protection Agency's (USEPA) Water Quality Planning and Management Regulations (40 CFR Part 130) require states to identify water bodies that violate state water quality standards and to develop Total Maximum Daily Loads (TMDLs) for such water bodies. A TMDL represents the total load of a pollutant that a water body can receive without violating state water quality standards. The TMDL process establishes the maximum allowable pollutant loading from both point and nonpoint sources for a water body, allocates the allowable load among the pollutant contributors, and provides a framework for taking actions to restore water quality.

### 1.1.2 Impairment Listing

Deep Run (VAN-E10R DPR01A00) was first listed as an impaired stream in 1996 based on VADEQ monitoring at station 3-DPR001.70 indicating that the swimmable use goal was not being met. Deep Run was further listed in 1998 and 2002 on Virginia's Section 303(d) Total Maximum Daily Load Priority List and Report (VADEQ, 2003a, b) due to water quality violations of the bacteria standard. The impaired portion of Deep Run, beginning at the confluence with Green Branch just downstream of the Route 752 bridge and continuing downstream approximately 4.83 miles to the confluence with the Rappahannock River is listed as impaired by fecal coliform bacteria on Virginia's 2002 list (VADEQ, 2003b). Deep Run is targeted for TMDL development and completion by 2004.

### 1.1.3 Watershed Location and Description

Part of the Rappahannock River basin, Deep Run watershed (Water body ID VAN-E10R) is located in Stafford County, Virginia and Fauquier County, Virginia (Figure 1.1). The southern portion of the main stem of Deep Run runs along the border between the two counties. The watershed area is 17,283 acres and is mainly forested (about 78%). The majority of the remaining 22% of the watershed area is divided among agricultural uses. Pasture/hay and cropland land uses comprise 20% and 1.3% of the watershed area, respectively. Deep Run flows south and discharges into the Rappahannock River (USGS Hydrologic Unit Code 02080103). The Rappahannock River discharges into the Chesapeake Bay.

### 1.1.4 Pollutant of Concern

Pollution from both point and nonpoint sources can lead to fecal coliform bacteria contamination of water bodies. Fecal coliform bacteria are found in the intestinal tract of warm-blooded animals; consequently, fecal waste of warm-blooded animals contains fecal coliform. Even though most fecal coliform are not pathogenic, some forms can be harmful to human health and their presence in water indicates recent contamination by fecal material. Because fecal material may contain pathogenic organisms, water bodies with fecal coliform counts may



also contain pathogenic organisms. For recreational activities involving contact with water, such as boating and swimming, health risks increase with increasing fecal coliform counts. If the fecal coliform concentration in a water body exceeds state water quality standards, the water body is listed for violation of the state fecal coliform standard for contact recreational uses. As discussed in Section 1.2.2, Virginia has adopted an *Escherichia coli* (*E. coli*) standard for water quality. The concentration of *E. coli* (a subset of the fecal coliform group) in water is considered to be a better indicator of pathogenic exposure than the concentration of the entire fecal coliform group in the water body.

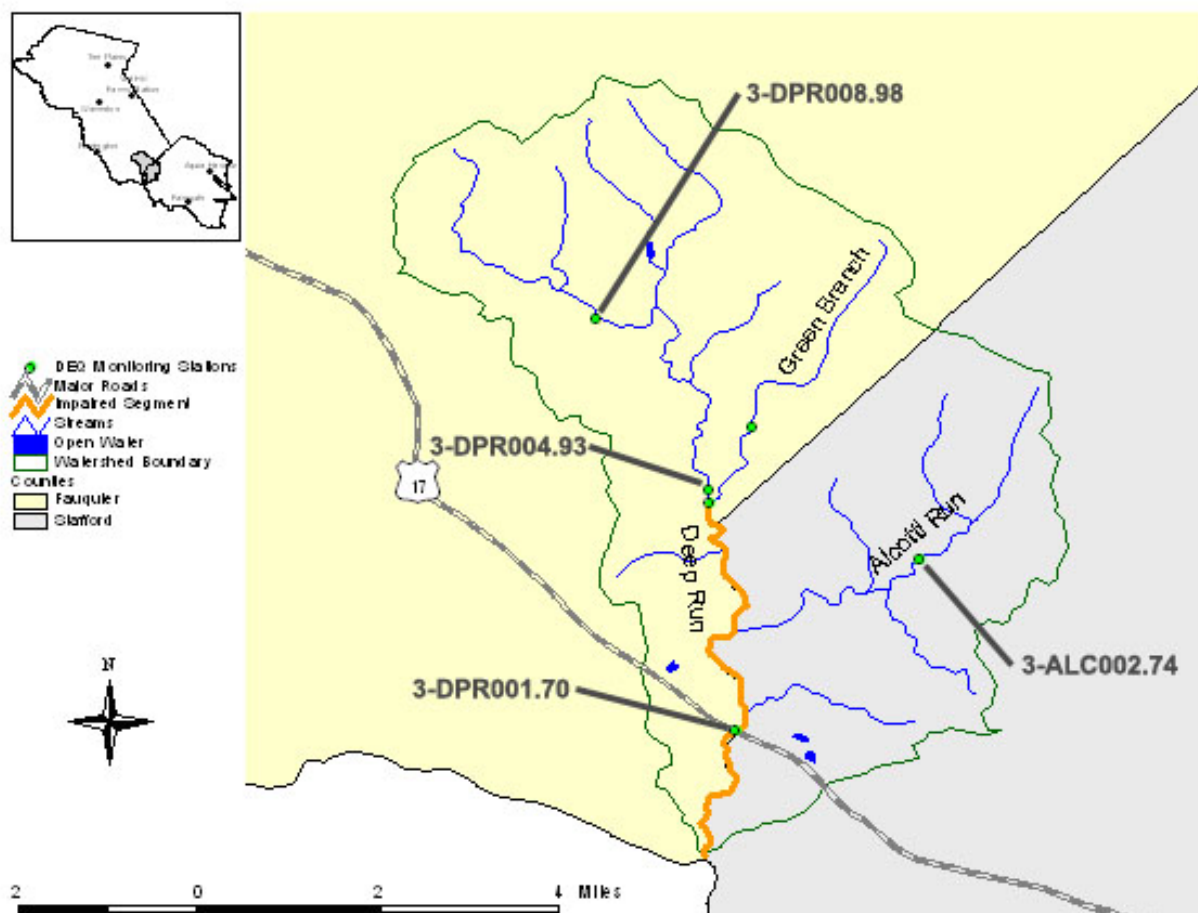


Figure 1.1. Location of the Deep Run watershed (VADEQ, 2004).

## 1.2 Designated Uses and Applicable Water Quality Standards

### 1.2.1 Designation of Uses (9 VAC 25-260-10)

“A. All state waters are designated for the following uses: recreational uses (e.g., swimming and boating); the propagation and growth of a balanced indigenous population of aquatic life, including game fish, which might reasonably be expected to inhabit them; wildlife; and the production of edible and marketable natural resources (e.g., fish and shellfish).”

The goal of the Clean Water Act is that all streams should be suitable for recreational uses, including swimming and fishing. **Fecal coliform and Escherichia coli (*E. coli*) bacteria** are used to indicate the presence of pathogens in streams supporting the **swimmable use goal**. Bacteria in Deep Run exceed the fecal coliform criterion.

### **1.2.2 Bacteria Standard (9 VAC 25-260-170)**

USEPA has recommended that all states adopt an *E. coli* or enterococci standard for fresh water and enterococci criteria for marine waters, because there is a stronger correlation between the concentration of these organisms (*E. coli* and enterococci) and the incidence of gastrointestinal illness than there is with fecal coliform. *E. coli* and enterococci are both bacteriological organisms that can be found in the intestinal tract of warm-blooded animals and are subsets of the fecal coliform and fecal streptococcus groups, respectively. In line with this recommendation, Virginia adopted and published revised bacteria criteria on June 17, 2002. The revised criteria became effective on January 15, 2003. As of that date, the *E. coli* standard described below applies to all freshwater streams in Virginia. Additionally, prior to June 30, 2008, the interim fecal coliform standard must be applied at any sampling station that has fewer than 12 samples of *E. coli*.

For a non-shellfish water body to be in compliance with Virginia's revised bacteria standards (as published in the Virginia Register Volume 18, Issue 20) the following criteria shall apply to protect primary contact recreational uses (VADEQ, 2000):

- **Interim Fecal Coliform Standard:** Fecal coliform bacteria shall not exceed a geometric mean of 200 fecal coliform bacteria per 100 mL of water for two or more samples over a calendar month nor shall more than 10% of the total samples taken during any calendar month exceed 400 fecal coliform bacteria per 100 mL of water.
- **Escherichia coli Standard:** *E. coli* bacteria concentrations for freshwater shall not exceed a geometric mean of 126 counts per 100 mL for two or more samples taken during any calendar month and shall not exceed an instantaneous single sample maximum of 235 cfu/100mL.

During any assessment period, if more than 10% of a station's samples exceed the applicable standard, the stream segment associated with that station is classified as impaired and a TMDL must be developed and implemented to bring the segment into compliance with the water quality standard. The original impairment to Deep Run was based on violations of an earlier fecal coliform standard that included a numeric single sample maximum limit of 1000 cfu/100 mL. The bacteria TMDL for these impaired segments was developed to meet the *E. coli* standard. As recommended by VADEQ, the modeling was conducted with fecal coliform inputs, and then a translator equation developed by the VADEQ was used to convert the output of the model to *E. coli*.

## **Chapter 2. Watershed Characterization**

### **2.1 Water Resources**

The Deep Run watershed was subdivided into eight sub-watersheds for fecal coliform modeling purposes, as discussed in Section 4.2. The main branch of Deep Run runs for 10.5 miles from the headwaters to the confluence with the Rappahannock River. Deep Run is a perennial stream with a trapezoidal channel cross-section. Aquifers in this watershed are overlain by limestone (VWCB, 1985). Depth to the water table is generally in excess of 6 feet (SCS, 1974).

### **2.2 Ecoregion**

The Deep Run watershed is split about evenly between the Piedmont and Northern Piedmont Level III Ecoregions. The Piedmont Ecoregion is predominantly wooded and consists of irregular plains, low rounded hills and ridges, shallow valleys, and scattered monadnocks (Woods et al., 1999). This ecoregion is a transitional area between the mostly mountainous ecoregions of the Appalachians to the west and the lower and more level ecoregions of the coastal plain to the east (Woods et al., 1999).

The Northern Piedmont Ecoregion consists primarily of low rounded hills, irregular plains, and open valleys and is underlain by metamorphic, igneous, and sedimentary rocks. The natural vegetation was mostly Appalachian Oak Forest (dominated by white and red oaks) (Woods et al., 1999).

### **2.3 Soils and Geology**

The Deep Run watershed is located within the Piedmont physiographic province. This province typically exhibits gently rolling hills and deeply weathered and poorly exposed bedrock.

The main soil map units found in the Deep Run watershed are the Nason-Elioak-Manor soil association and the Croton, Goldvein, and Manteo series (SCS, 1974). The Nason-Elioak-Manor association soils are generally deep, well-drained to excessively drained with dominantly silt or clay subsoils. Both seasonal water table and bedrock depths are greater than five feet and are typically gently sloping to strongly sloping. They are formed from weathered micaceous schist. The Croton series soils are deep and poorly drained, and are found on the upland areas. The Croton soils are typically formed over sandstone, siltstone, or shale (NRCS, 2004). The Goldvein series soils are deep and moderately well drained with slow permeability, formed from weathered quartz monzonite, pegmatites, and other granites. The Manteo series soils are shallow and very well drained, almost to excess (NRCS, 2004).

### **2.4 Climate**

The climate of the Deep Run watershed is characterized based on the meteorological observations assembled by the Southeast Regional Climate Center for the Warrenton, Virginia station. The weather station is located about 15 miles northwest of the Deep Run watershed.

Average annual precipitation is 40.94 inches with 54% of the precipitation occurring during the crop-growing season (May-October) (SERCC, 2004). Average annual snowfall is 22.3 inches with the highest snowfall occurring during January (SERCC, 2004). Average annual daily temperature is 54.3°F. The highest average daily temperature of 75.1°F occurs in July while the lowest average daily temperature of 31.6°F occurs in January (SERCC, 2004).

## **2.5 Existing Land Use**

Forested areas represent the main land use category in the Deep Run watershed, covering 78.0% of the total watershed area. Agricultural land uses constitute the majority of the remaining watershed area, with pasture and cropland land use categories making up 13.2% and 7.9%, respectively. Residential development and water cover the balance of the watershed area.

## **2.6 Future Land Use**

The Stafford County comprehensive plan does not identify any future urban development areas or similar plans for that side of the watershed (Stafford County, 2004). Rather, all developable land in that portion of Stafford County is zoned for agricultural use which dictates a minimum 3-acre lot size for single family dwellings.

Similarly, a review of the Fauquier County Comprehensive Plan for 1992-2010 did not reveal specific plans to promote the development of the Deep Run watershed based on designated villages or development areas (Fauquier County, 2004). The revised future land use data currently under development were not available for review during this study.

It is our understanding that no major zoning changes are planned by either county that would result in accelerated development of the watershed. For purposes of this study, it was assumed that residential development in the Deep Run watershed will continue at the current rate.

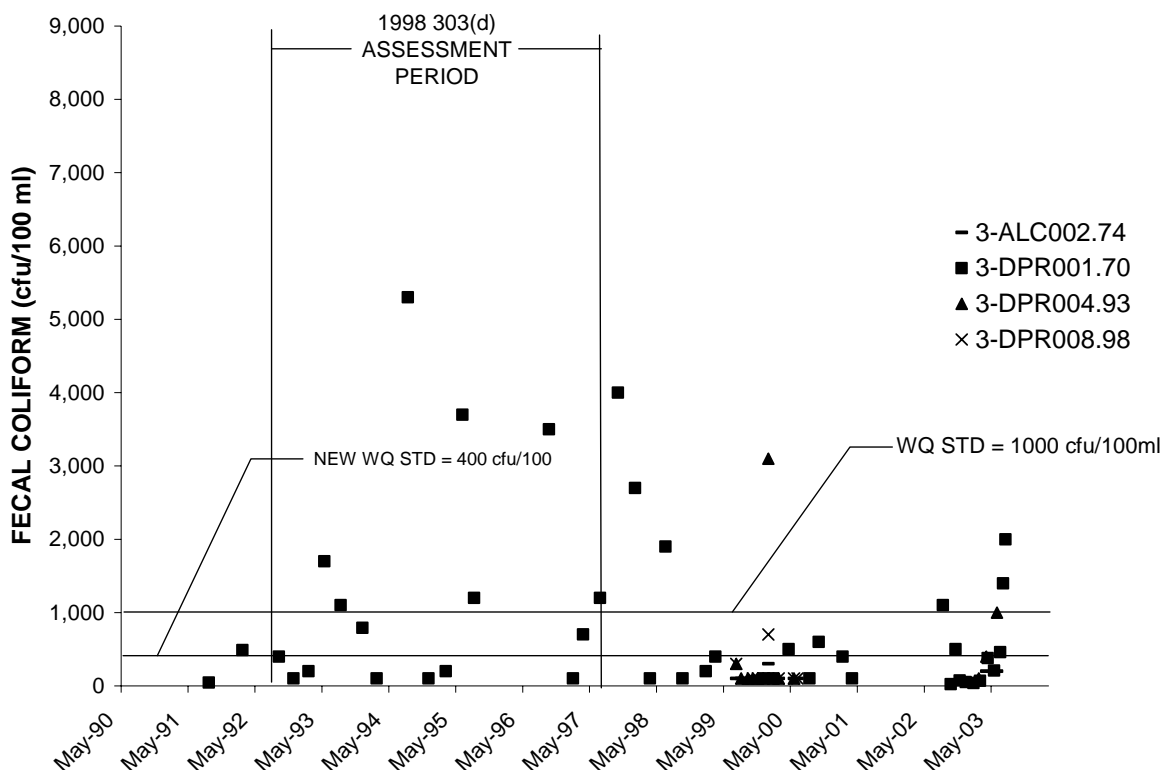
## **2.7 Water Quality Data**

### **2.7.1 Historic Data for Fecal Coliform**

Of the 16 water quality samples collected from July 1992 through June 1997 (the 1998 Section 303(d) 5-year listing period) near the outlet of the watershed, 44% of the samples exceeded the then-applicable instantaneous standard of 1,000 cfu/100 mL. Consequently, this segment of Deep Run was determined as not supporting the Clean Water Act's Swimming Use Support Goal for the 1998 Section 305(b) report and was included in the 1998 Section 303(d) list (VADEQ, 2003).

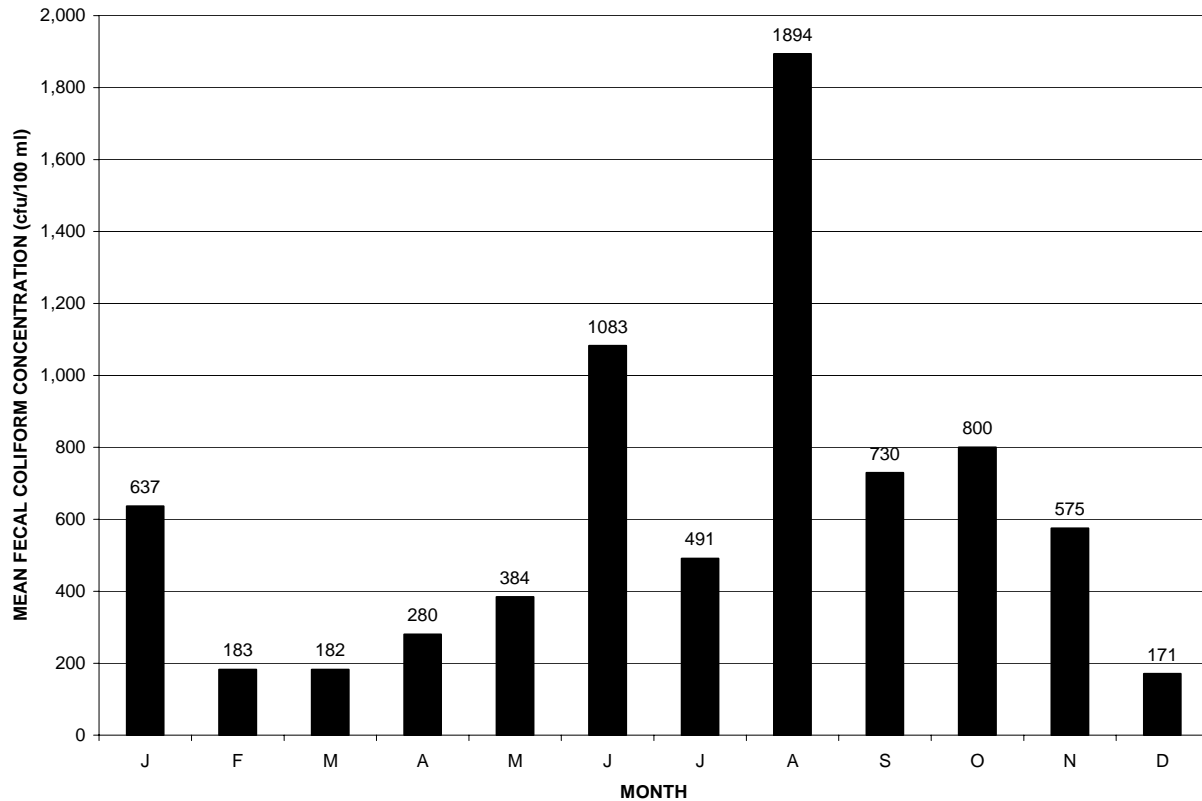
VADEQ personnel monitored pollutant concentrations at the Deep Run watershed outlet (Station ID No. 3-DPR001.70). Monitoring data with corresponding 6-day antecedent precipitation used in assessment of Deep Run, as well as in this study, are included in Appendix A. Time series data of fecal coliform concentration at all bacteria monitoring stations in the Deep Run watershed from 1990 through the most recent data collected at the time this report was

written are shown in Figure 2.1. The Most Probable Number (MPN) method was used for analyzing water samples for fecal coliform concentration.



**Figure 2.1. Fecal coliform concentration in Deep Run watershed.**

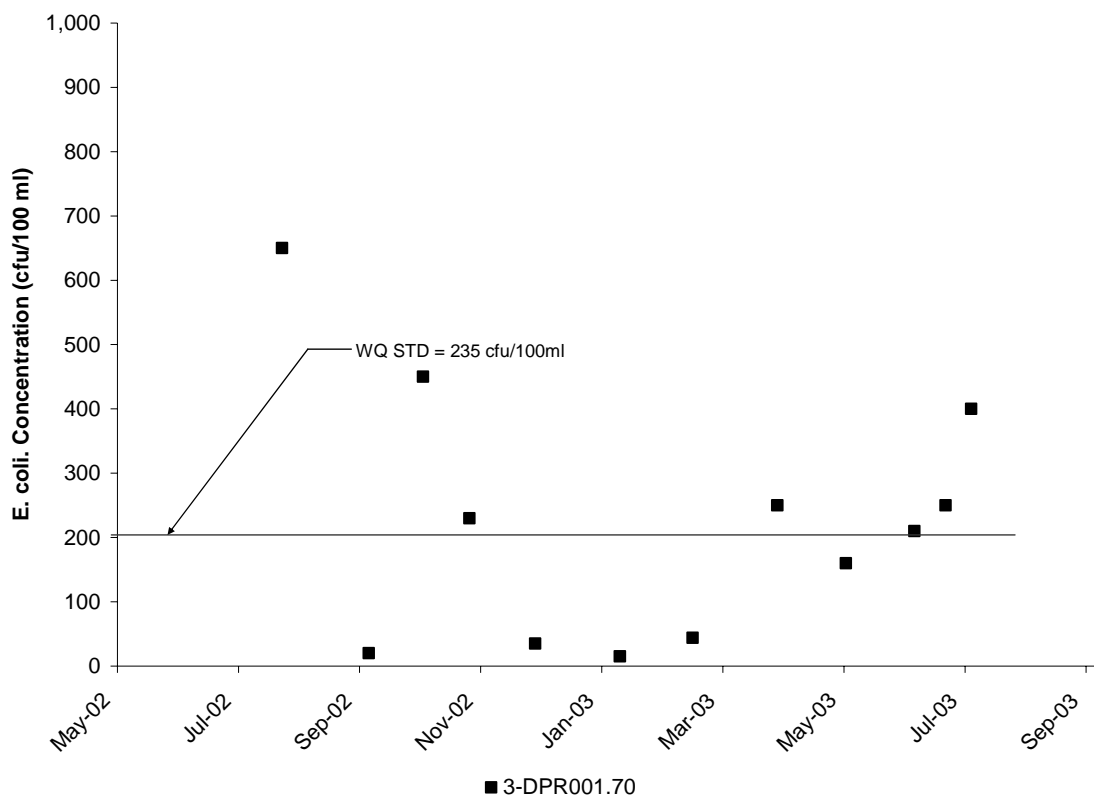
Seasonal variability of fecal coliform concentration in the stream network was evaluated by plotting the mean monthly fecal coliform concentration values (Figure 2.2). Mean monthly fecal coliform concentration values were determined as the average of six to 13 values for each month; the number of values varied according to the available number of samples for each month in the 1976 to 2003 period of record. The data indicate that higher in-stream fecal coliform concentrations occur during the summer months, particularly in August. The lower concentrations occurred in the winter and spring months, except for January. It should be noted that due to the upper cap (8,000 cfu/100 mL) and lower cap (100 cfu/100ml) imposed on the fecal coliform count, the actual counts could be higher or lower in cases where fecal coliform levels are equal to these level limits, therefore changing the averages shown in Figure 2.2.



**Figure 2.2. Impact of seasonality on fecal coliform concentrations in Deep Run watershed.**

### **2.7.2 Historic Data for *E. coli***

VADEQ staff also examined water samples collected at station 3-DPR001.70 for their concentration of *E. coli*. This analysis was conducted concurrently with other monthly testing at the station from August 2002 through July 2003, with twelve samples analyzed. Of these twelve samples, five (42%) exceeded the single maximum water quality standard. Those data are shown in Figure 2.3.



**Figure 2.3. *E. coli* concentration in Deep Run watershed.**

### **2.7.3 Historic Data for Bacteria Source Tracking**

The results from 12 monthly bacteria source tracking (BST) samples collected at station 3-DPR001.70 were received at the time this report was prepared. The BST analysis was performed by MapTech, Inc. as a separate study. The results of the BST analysis provide a measure of the relative contribution of bacteria sources to the bacteria concentration found in the water samples. The bacteria sources were lumped into four categories: wildlife, human, livestock, and pet. Data resulting from the BST study are included in Appendix B. A discussion of the BST results provided by VADEQ indicates there is 90% confidence that the indicated proportions for each sample are within 15% of the sampled population (Appendix B). These data represent a brief glimpse of bacteria concentration in Deep Run and may not be representative of long-term conditions in the stream.

The analysis in the BST report also included a test of statistical significance, providing an indication of presence or absence of contribution from a particular source. The presence/absence use of these data is most appropriate for use in this study due to statistical confidence, with presence defined as any proportional contribution greater than 15%. Table 2.1 summarizes the results of the presence/absence analysis of the BST data. The BST data were used to verify modeling methods and assumptions.

**Table 2.1. Presence/absence analysis of bacteria sources at station 3DPR001.70 in Deep Run watershed.**

<b>Bacteria Source</b>	<b>Frequency of Presence in All Samples<sup>1</sup></b>	<b>Frequency of Presence in Samples Exceeding Water Quality Standards<sup>2</sup></b>
Wildlife	92%	100%
Human	25%	0%
Livestock	67%	100%
Pet	75%	67%

1 – This is a measure of the number of times the source is present in all 12 samples.

2 – This is a measure of the number of times the source was present in samples that exceeded either the fecal coliform or *E. coli* instantaneous standard.

Fecal coliform and *E. coli* enumerations were also performed on the BST samples. These data can also be found in Appendix B. Thirty-eight percent of the samples exceeded both fecal coliform and *E. coli* standards. It should be noted that most of the samples that violated water quality standards were collected between June 2003 and August 2003. Though discharge was not measured when samples were collected, most of the violations were observed during the wetter portion of the sample collection period.



## Chapter 3. Bacteria Source Assessment

Potential bacteria sources in the Deep Run watershed were assessed using multiple approaches, including information from VADEQ, Virginia Department of Conservation (VADCR), Virginia Department of Game and Inland Fisheries (VADGIF), Virginia Cooperative Extension (VCE), Virginia Department of Health (VDH), Fauquier and Stafford County Planning and GIS departments, Virginia Poultry Federation, Natural Resources Conservation Service (NRCS), Virginia Department of Agricultural and Consumer Services (VDACS), John Marshall Soil and Water Conservation District, Tri-County/City Soil and Water Conservation District, public participation, farmer interviews, watershed reconnaissance and monitoring, published information, and professional judgment. The gathered information was used to estimate source populations and their associated bacteria loads throughout the Deep Run watershed, forming the basis for model development and analysis of allocation scenarios (Table 3.1). The following sections discuss available information and methods used to estimate bacteria loads for each modeling segment.

**Table 3.1. Sources of bacteria in the Deep Run watershed.**

Source Category	Source / Animal Type	Applied To
Human and Pets	Permitted Discharges	Stream Reach
	Straight Pipes	Stream Reach
	Failing Septic Systems	Land
	Biosolids Applications	Land
	Dogs / Cats	Land
Agricultural	Dairy Cattle	Land, Stream Reach
	Beef Cattle	Land, Stream Reach
	Horses	Land
	Other Livestock	Land
Wildlife	Deer	Land, Stream Reach
	Raccoon	Land, Stream Reach
	Muskrats	Land, Stream Reach
	Beavers	Land, Stream Reach
	Turkeys	Land, Stream Reach
	Geese	Land, Stream Reach
	Ducks	Land, Stream Reach

### 3.1 Permitted Discharges

Virginia Pollutant Discharge Elimination System (VPDES) and Phase II Municipal Separate Storm Sewer System (MS4) permits were reviewed to determine if any facilities discharge within the Deep Run watershed. There are no individual or general VPDES or MS4 permit discharges in the watershed.

## 3.2 Humans and Pets

Stafford and Fauquier County staff indicate that no part of the Deep Run watershed is served by municipal sewer. Wastewater from all households within the watershed is treated on site by traditional sewage handling and disposal systems.

The Deep Run watershed has an estimated population of 2,524 people (895 households at an average of 2.82 people per household (UCSB, 2000); actual people per household varies among sub-watersheds). Humans produce  $1.95 \times 10^9$  cfu/day-person (Geldreich et al., 1978), resulting in a total fecal coliform production of  $4.92 \times 10^{12}$  cfu/day ( $1.80 \times 10^{15}$  cfu/year).

Bacteria from humans and pets can be transported to streams from failing septic systems, straight pipes discharging directly into streams, biosolids applications to pasture and cropland, or deposition of pet waste on residential land.

### 3.2.1 Failing Septic Systems

Septic systems are designed to filter septic tank effluent through the soil allowing removal of bacteria and nutrients from the wastewater. Septic system failure is manifested by the rise of effluent to the soil surface. It was assumed that no die-off occurred once effluent containing fecal coliform reached the soil surface. Surface runoff can transport the effluent containing fecal coliform to receiving waters.

Each unsewered household was classified into one of three age categories (pre-1967, 1967-1987, and post-1987) based on when it was constructed. An average number of people per household and the number of houses and people in each subwatershed in 2003 were established using 2000 U.S. census data (UCSB, 2000) and growth trends (Knapp et. al., 2003). Households present in 1987 were identified within each subwatershed by digitizing their locations on 1987 USGS 7.5-minute topographic maps, and the same average occupancy identified for 2003 was used to estimate watershed population in 1987. The population and number of houses present in each subwatershed in 1967 were estimated by using historic census data to establish a growth trend that was then applied to the 1987 data. The pre-1967 era houses were defined using the estimated 1967 data. The 1967-1987 era houses were defined by subtracting the 1967 era houses from those identified as being present in 1987. The post-1987 era houses were defined by subtracting the houses identified as being present in 1987 from those present in 2003.

Professional judgment was applied in assuming that septic system failure rates for houses in the pre-1967, 1967-1987, and post-1987 age categories were 40, 20, and 3%, respectively (BSE, 2003). Estimates of these failure rates were also supported by the Holmans Creek Watershed Study which found that over 30% of all septic systems checked in the watershed were either failing or not functioning at all (SAIC, 2001).

Daily total fecal coliform load to the land from a failing septic system in a particular sub-watershed was determined by multiplying the average household occupancy rate for that subwatershed by the per capita fecal coliform production rate of  $1.95 \times 10^9$  cfu/day (Geldreich et al., 1978). Hence, the total fecal coliform loading to the land from a single failing septic system

in a subwatershed with an occupancy rate of 2.82 persons/household was  $5.50 \times 10^9$  cfu/day. Transport of some portion of the fecal coliform to a stream by runoff may occur during storm events. The number of failing septic systems in the watershed is given in Table 3.3.

### **3.2.2 *Straight Pipes***

Houses that deliver a waste load directly to the stream, or straight pipes, were estimated by identifying those houses located within 150 feet of streams in the pre-1967 and 1967-1987 age categories. This method yielded four houses that potentially could be classified as straight pipes. County health department staff indicated they were not aware of the presence of any straight pipes. Field reconnaissance revealed that significantly more than four houses were located within 150 feet of the stream network. When asked for input on the matter, TAC members indicated that an estimate of one to two straight pipes per subwatershed would be more accurate based on local knowledge. This estimate was used for modeling purposes. Considering all data and feedback, it was estimated that a total of eleven straight pipes with no more than two in any given subwatershed are present in the watershed (Table 3.3).

### **3.2.3 *Biosolids***

According to VDH records, Class B biosolids were applied to 189 acres in 2000 and zero acres in 2001 in Fauquier County. Likewise, biosolids were applied to 2,050 acres in 2000 and 3,281 acres in Stafford County. Application rates, bacteria concentrations, and spatial distribution of application sites within the Deep Run watershed were not available. To estimate biosolids applications within each Deep Run subwatershed, the average annual biosolids application areas for counties were divided by the total pasture acreage in the county, and then this rate was distributed based on the pasture acreage in each subwatershed. A maximum application rate of 15 dry tons/acre was used to estimate the amount applied. Although Class B biosolids are permitted to contain fecal coliform concentrations of  $2.0 \times 10^6$  cfu/g (VDH, 1997), values reported by treatment plants are typically lower than this value. For this study, VDH staff indicated that the primary source for biosolids was Blue Plains, the largest wastewater treatment plant in the Washington D.C. metropolitan area. The fecal coliform density of biosolids from Blue Plains is estimated to be less than 2,000 cfu/g (MapTech, 2002). Therefore, an average fecal coliform density of 2,000 cfu/g was used for bacteria loading calculations. Table 3.2 shows the estimated average annual biosolids application amount for each subwatershed.

**Table 3.2. Estimated average annual biosolids application amount for each subwatershed in the Deep Run watershed.**

<b>Subwatershed</b>	<b>Biosolids Applied (dry tons / year)</b>
D-1	89.5
D-2	33.0
D-3	52.8
D-4	68.7
D-5	106.6
D-6	61.4
D-7	127.5
D-8	15.5
<b>Total</b>	<b>555.0</b>

### **3.2.4 Pets**

According to the American Veterinary Medical Association (AVMA), there are on average 0.53 dogs per household and 0.60 cats per household in the U.S. (AVMA, 1997). During visits to the watershed, the number of dogs and cats observed appeared to be significantly higher than these published figures. Consultation with the TAC revealed that, due to the rural nature of the area, a better estimate of the pet populations in the watershed would be double the published figures. Therefore, population densities of 1.0 and 1.2 animals per household were used to estimate dogs and cats, respectively. All pets were combined for modeling purposes into one category of “pet population.” Using these density estimates, there are an estimated 1,966 pets in the Deep Run watershed. The maximum typical fecal coliform production for both dogs and cats is  $5.0 \times 10^9$  cfu/day-animal (Keeling, 2003), and the typical ranges overlap significantly. The pet population was estimated to produce  $4.5 \times 10^8$  cfu/day-animal based on these published values. The total bacteria production attributed to pets in the Deep Run watershed is  $8.8 \times 10^{11}$  cfu/day ( $3.2 \times 10^{14}$  cfu/yr). The pet population distribution among the subwatersheds is listed in Table 3.3. Pet waste is generated in the residential land use type. Bacteria loading to streams from pet waste can result from surface runoff transporting bacteria from residential areas.

**Table 3.3. Estimated human population, number of unsewered houses by age category, number of failing septic systems, number of straight pipes, and pet population in Deep Run watershed.**

Subwatershed	Human Population	Unsewered Houses in Each Age Category (no.)			Failing Septic System (no.)	Straight Pipes (no.)	Pet Population <sup>a</sup>
		Pre-1967	1967 - 1987	Post-1987			
D-1	146	12	25	15	10	1	114
D-2	340	28	58	34	24	1	265
D-3	340	28	58	35	24	2	265
D-4	307	25	52	32	21	1	239
D-5	329	27	56	34	23	2	257
D-6	511	42	87	52	36	1	399
D-7	524	43	91	52	37	2	408
D-8	24	2	4	3	2	1	19
<b>Total</b>	<b>2,521</b>	<b>207</b>	<b>431</b>	<b>257</b>	<b>177</b>	<b>11</b>	<b>1,966</b>

<sup>a</sup>Calculated from average of 2.2 pets per household.

### 3.3 Livestock Sources

In the Deep Run watershed, bacteria from livestock waste can be directly excreted to the stream, or it can be transported to the stream by surface runoff from animals depositing waste on pastures or from applying collected waste on crop and hay land. Livestock populations in the Deep Run watershed were estimated based on Virginia Agriculture Statistics Service (VASS) data and communication with staff from SWCDs, NRCS, VADCR, VCE, VDACS, and local producers.

#### 3.3.1 Cattle

At present there are no dairy farms in the watershed, based on information obtained from visual observation of the watershed and from the data sources indicated in Section 3.3. Prior to October 1998, there was one dairy operation within the watershed. Based on communication with regulators and the gentleman who operated the dairy, it was determined that there were 125 milk cows, 50 dry cows, and 125 heifers at this dairy prior to closure. The dairy cattle population was distributed among the sub-watersheds based on the location of the dairy farm (Table 3.4). Beef cattle in the watershed (263 pairs) included cow/calf and feeder operations.

**Table 3.4. Distribution of dairy cattle, dairy operations, and beef cattle among sub-watersheds in Deep Run watershed.**

Subwatershed	Dairy Cattle <sup>a</sup>	No. of Dairy Operations	Beef Cattle (pairs)
D-1	0	0	48
D-2	0	0	18
D-3	0	0	28
D-4	0	0	37
D-5	0	0	30
D-6	0	0	17
D-7	300 <sup>b</sup>	1 <sup>b</sup>	79 <sup>b</sup> (154) <sup>c</sup>
D-8	0	0	6
<b>Total</b>	<b>300</b>	<b>1</b>	<b>263</b>

<sup>a</sup>Consists of the milking herd, dry cows, and heifers. Sole dairy ceased operations in October 1998.

<sup>b</sup>Numbers prior to October 1998.

<sup>c</sup>Number in parentheses constitutes numbers after October 1998.

Cattle spend varying amounts of time in confinement, loafing lots, streams, and pasture depending on the time of year and type of cattle (i.e., milk cow versus heifer). Accordingly, the proportion of bacteria deposited in any given land area varies throughout the year. Based on discussions with SWCDs, NRCS, VADCR, VCE, and local producers, the following assumptions and procedures were used to estimate the distribution of cattle (and thus their manure) among different land use types and in the stream:

- Cows are confined according to the schedule given in Table 3.5.
- When cattle are not confined, they spend their time on pasture and in loafing lots, where applicable.
- Pasture 1 (improved pasture/hay land) stocks twice as many cows per unit area as pasture 2 (unimproved pasture/grazed woodlands), which stocks twice as many cows per unit area as pasture 3 (overgrazed pasture).
- Cows on pastures that are contiguous to streams have stream access.
- Cows with stream access spend varying amounts of time in the stream during different seasons (Table 3.5). Cows spend more time in the stream during the three summer months to protect their hooves from hornflies, among other things.
- Thirty percent of cows in and around streams directly deposit fecal coliform into the stream. The remaining 70% of the manure is deposited on pastures.

**Table 3.5. Time spent by cattle in confinement and in the stream in Deep Run watershed.**

Month	Time Spent in Confinement (%)		Time Spent in Stream (hours/day)*
	Milking	Dry Cows, Heifers, and Beef Cattle	
January	75	40	0.50
February	75	40	0.50
March	40	0	0.75
April	30	0	1.00
May	30	0	1.50
June	30	0	3.50
July	30	0	3.50
August	30	0	3.50
September	30	0	1.50
October	30	0	1.00
November	40	0	0.75
December	75	40	0.50

\* Time spent in and around the stream by cows that have stream access.

The time cattle spend each month in various land uses or a given stream reach was estimated based on typical agricultural practice, and adjusted to reflect feedback from TAC members and agricultural producers. Using these data describing where cattle spend their time, the cattle and their resulting bacteria loads were distributed among the land uses for modeling purposes. The resulting numbers of cattle in each land use type as well as in the stream for all sub-watersheds are given in Table 3.6 for dairy cattle and in Table 3.7 for beef cattle.

**Table 3.6. Distribution of the dairy cattle<sup>a</sup> population in the Deep Run watershed.**

Month	Confined	Pasture 1	Pasture 2	Pasture 3	Stream <sup>b</sup>	Loafing <sup>c</sup>
January	164	84	21	5	0.012	27
February	164	84	21	5	0.012	27
March	50	142	36	9	0.031	64
April	38	143	36	9	0.042	74
May	38	143	36	9	0.063	74
June	38	143	36	9	0.148	74
July	38	143	36	9	0.148	74
August	38	143	36	9	0.148	74
September	38	143	36	9	0.063	74
October	38	143	36	9	0.042	74
November	50	142	36	9	0.031	64
December	164	84	21	5	0.012	27

<sup>a</sup>Includes milk cows, dry cows, and heifers.

<sup>b</sup>Number of dairy cattle defecating in stream.

<sup>c</sup>Milk cows in loafing lot.

**Table 3.7. Distribution of the beef cattle population (pairs) in the Deep Run watershed.**

Month	Confined	Pasture 1	Pasture 2	Pasture 3	Stream*	Loafing
January	0	200	50	13	0.043	0
February	0	200	50	13	0.043	0
March	0	200	50	13	0.065	0
April	0	200	50	13	0.086	0
May	0	200	50	13	0.129	0
June	0	200	50	13	0.301	0
July	0	200	50	13	0.301	0
August	0	200	50	13	0.301	0
September	0	200	50	13	0.129	0
October	0	200	50	13	0.086	0
November	0	200	50	13	0.065	0
December	0	200	50	13	0.043	0

\*Number of beef cattle defecating in stream.

### 3.3.1.1 Direct Manure Deposition in Streams

Direct manure loading to streams is due to both dairy (Table 3.6) and beef cattle (Table 3.7) defecating in the stream. However, only cattle on pastures contiguous to streams which have not been fenced off have stream access. Manure loading increases during the warmer months when cattle spend more time in water, compared to the cooler months. Average annual manure loading directly deposited by cattle in the stream for the watershed is 4,432 lb. Fecal coliform loading due to cows defecating in the stream, averaged over the year, is  $5.4 \times 10^9$  cfu/day ( $2.0 \times 10^{12}$  cfu/year). Part of the fecal coliform deposited in the stream stays in the dissolved form while the remainder adsorbs to the sediment in the streambed. Under base flow



conditions, it is likely that dissolved fecal coliform bacteria are the primary form transported with the flow. Sediment-bound bacteria are likely to be re-suspended and transported to the watershed outlet under high flow conditions. For this TMDL, the dissolved form of bacteria was modeled and re-suspension of sediment-bound bacteria was accounted for through calibration (see Chapter 4). Die-off of fecal coliform in the stream depends on sunlight, predation, turbidity, and other environmental factors.

#### 3.3.1.2 Direct Manure Deposition on Pastures

Dairy (Table 3.6) and beef (Table 3.7) cattle that graze on pastures but do not deposit in streams contribute the majority of fecal coliform loading on pastures. Manure loading on pasture was estimated by multiplying the total number of each type of cattle (milk cow, dry cow, heifer, and beef) on pasture by the amount of manure it produced per day. The total amount of manure produced by all types of cattle was divided by the pasture acreage to obtain manure loading (lb/ac-day) on pasture. Fecal coliform loading (cfu/ac-day) on pasture was calculated by multiplying the manure loading (lb/ac-day) by the fecal coliform content (cfu/lb) of the manure. Since the confinement schedule of the cattle changes with season, manure and fecal coliform loading on pasture also change with season.

Pasture 1, pasture 2, and pasture 3 have average annual cattle manure loadings of 5,675, 2,838, and 1,489 lb/ac-year, respectively. The loadings vary because the stocking rate varies with pasture type, with improved pasture able to stock the most cattle. Fecal coliform loadings from cattle, averaged over the year, are  $2.82 \times 10^{12}$ ,  $1.73 \times 10^{12}$ , and  $7.20 \times 10^{11}$  cfu/ac-year for pastures 1, 2, and 3, respectively. Fecal coliform bacteria deposited on the pasture surface are subject to die-off due to desiccation and ultraviolet (UV) radiation. Runoff can transport part of the remaining fecal coliform to receiving waters.

#### 3.3.1.3 Land Application of Liquid Dairy Manure

A typical milk cow weighs 1,400 pounds and produces 17 gallons of liquid manure daily (ASAE, 1998). Based on the monthly confinement schedule (Table 3.5) and the number of milk cows (Section 3.3.1), annual liquid dairy manure production in the watershed is 464,397 gallons. Based on per capita fecal coliform production of milk cows, the fecal coliform concentration in fresh liquid dairy manure is  $1.47 \times 10^9$  cfu/gal. Liquid dairy manure receives priority over other manure types (poultry litter and solid cattle manure) in application to land. Liquid dairy manure application rates are 6,600 and 3,900 gal/ac-year to cropland and pasture land use categories (BSE, 2003), respectively, with cropland receiving priority in application. Based on availability of land and liquid dairy manure, as well as the assumptions regarding application rates and priority of application, it was estimated that liquid dairy manure was applied to 50.3 acres (3.7%) of cropland. Because there was insufficient liquid dairy manure for cropland, no liquid dairy manure was applied to pasture.

The typical crop rotation in the watershed is a seven-year rotation with three years of corn-rye and four years of rotational hay (BSE, 2003). It was assumed that 50% of the corn acreage was under no-till cultivation. Liquid manure is applied to cropland during February through May (prior to planting) and in October-November (after the crops are harvested). For spring application to cropland, liquid manure is applied on the soil surface to rotational hay and

no-till corn and is incorporated into the soil for corn in conventional tillage. In fall, liquid manure is incorporated into the soil for cropland under rye and surface-applied to cropland under rotational hay. It was assumed that only 10% of the subsurface-applied fecal coliform was available for removal in surface runoff based on local knowledge. The application schedule of liquid manure (BSE, 2003) is given in Table 3.8. Dry cows and heifers were assumed to produce only solid manure.

**Table 3.8. Schedule of cattle waste application in Deep Run watershed.**

<b>Month</b>	<b>Liquid Manure Applied (%)<sup>*</sup></b>	<b>Solid Manure Applied (%)<sup>*</sup></b>
January	0	0
February	5	5
March	25	25
April	20	20
May	5	5
June	10	5
July	0	5
August	5	5
September	15	10
October	5	10
November	10	10
December	0	0

<sup>\*</sup> As percent of annual production.

#### 3.3.1.4 Land Application of Solid Manure

Solid manure produced by dry cows, heifers, and beef cattle during confinement is collected for land application. It was assumed that milk cows produce only liquid manure while in confinement. The number of cattle, their typical weights, amounts of solid manure produced, and fecal coliform concentration in fresh manure are given in Table 3.9.

Solid manure is last on the priority list for application to land (it falls behind liquid manure). The amount of solid manure produced in each sub-watershed was estimated based on the populations of dry cows, heifers, and beef cattle in the sub-watershed (Table 3.4) and their confinement schedules (Table 3.5). Solid manure from dry cows, heifers, and beef cattle exhibits different fecal coliform concentrations (cfu/lb) (Table 3.9). Hence, a weighted average fecal coliform concentration in solid manure was calculated based on the relative manure contribution from dry cows, heifers, and beef cattle (Table 3.9). Solid manure is applied at the rate of 12 tons/ac-year to both cropland and pasture, with priority given to cropland. As in the case of liquid manure, solid manure is only applied to cropland during February through May and the months of October and November.

Solid manure can be applied to pasture during the whole year except during December and January. The method of application of solid manure to cropland or pasture is assumed to be identical to the method of application of liquid dairy manure. The application schedule for solid

manure is given in Table 3.8. Based on availability of land and solid manure, as well as the assumptions regarding application rate, 16.3 acres (1.2%) of the cropland received solid manure application. Because there was insufficient solid manure for cropland, solid manure was not applied on pasture 1, pasture 2, or pasture 3.

**Table 3.9. Estimated population of dry cows, heifers, and beef cattle, typical weights, per capita solid manure production, fecal coliform concentration in fresh solid manure in individual cattle type, and weighted average fecal coliform concentration in fresh solid manure in Deep Run watershed.**

Type of Cattle	Population	Typical Weight (lb) <sup>a</sup>	Solid Manure Produced (lb/animal-day) <sup>a</sup>	Fecal Coliform Concentration in Fresh Manure ( $\times 10^8$ cfu/lb) <sup>a</sup>	Weighted Average Fecal Coliform Concentration in Fresh Manure ( $\times 10^8$ cfu/lb)
Dry Cow	50	1,400	115	2.17	4.11
Heifer	125	640	40.7	2.17	
Beef (pairs)	263	1,000	60	5.5	

<sup>a</sup>Source: BSE (2003)

### 3.3.2 Horses

The estimated number of horses in the Deep Run watershed is included in Table 3.10. The horse population in the watershed has risen significantly in the last several years. Horse populations will be estimated using data from the 2001 Virginia Equine Report produced by VASS. The number of horses inventoried in the report by county are as follows (VASS, 2002):

- Fauquier: 13,700
- Stafford: 1,300

The number of horses within the watershed was estimated by distributing the equine population evenly throughout all pasture in the respective county and determining the number of horses in the watershed based on pasture area in the watershed. The same method was used to determine the equine population in each subwatershed.

The typical horse produces  $4.2 \times 10^8$  cfu/day (VADCR, 2003). Therefore, the daily fecal coliform production by horses in the Deep Run watershed is  $1.20 \times 10^{11}$  cfu/day ( $4.4 \times 10^{13}$  cfu/year).

### 3.3.3 Other Livestock Sources

There are other livestock-related sources of bacteria within the watershed, including sheep, goats, and imported poultry litter. Sheep and goat populations were determined using VASS data and area-weighting the county populations using pasture areas in each subwatershed. The goat population was adjusted to reflect increases suggested by the TAC. The resulting sheep and goat populations are included in Table 3.10. The fecal coliform productions by sheep and goats are  $1.2 \times 10^{10}$  cfu/day-animal unit and  $2.8 \times 10^{10}$  cfu/day-animal unit, respectively (ASAE, 1998). This results in a daily load in the watershed from sheep and

goats of  $1.03 \times 10^{12}$  cfu/day ( $3.76 \times 10^{14}$  cfu/year) and  $1.18 \times 10^{12}$  cfu/day ( $4.31 \times 10^{14}$  cfu/year), respectively, after accounting for local animal weights.

VADEQ staff provided estimates of poultry litter being imported into Stafford and Fauquier counties. No significant amount of poultry litter is imported to Stafford County, while about 600 tons are imported to Fauquier County each year. These data were proportioned among pasture areas in the county and watershed to determine poultry litter imported into the Deep Run watershed. Approximately 14 tons of poultry litter is being imported into the watershed from other watersheds each year for fertilizer and soil amendment. The poultry litter was then distributed among the subwatersheds in the same fashion. The imported poultry litter results in a total bacteria load of  $1.49 \times 10^{13}$  cfu/year in the Deep Run watershed.

**Table 3.10. Other livestock populations by subwatershed in the Deep Run watershed.**

Subwatershed	Horses	Sheep	Goats
D-1	53	4	10
D-2	20	2	10
D-3	31	2	10
D-4	41	3	5
D-5	44	0	5
D-6	25	0	5
D-7	64	3	5
D-8	8	1	5
<b>Total</b>	<b>286</b>	<b>15</b>	<b>55</b>

### 3.4 Wildlife

Fecal coliform production rates for wildlife species considered in this study are listed in Table 3.13. The total wildlife fecal coliform production each year in the Deep Run watershed is  $5.11 \times 10^{14}$  cfu/yr.

Wildlife fecal coliform contributions can be from excretion of waste on land and from excretion directly into streams. Information provided by VADGIF, USF&WS, and watershed residents was used to estimate wildlife populations. Wildlife species that were found in quantifiable numbers in the watershed included deer, raccoon, muskrat, beaver, wild turkey, goose, and wood duck. Preferred habitat, habitat area, and population density were determined for each species (Table 3.11).

Professional judgment was used in estimating the percent of each wildlife species defecating directly into streams based upon their habitat (Table 3.11). Fecal matter produced by deer that is not directly deposited in streams is distributed among pastures and forest. Raccoons deposit their waste in streams and forests. Muskrats deposit their waste in streams and pastures.

Fecal loading from wildlife was estimated for each sub-watershed. The wildlife populations were distributed among sub-watersheds based on habitat descriptions included in

Table 3.11, and further details of the wildlife habitat were used to distribute the populations among the sub-watersheds. For example, the deer population was evenly distributed across the watershed, whereas the 66 feet buffer around streams and impoundments determined the muskrat population. Therefore, a sub-watershed with more stream length and impoundments would have more muskrats than a sub-watershed with shorter stream length and fewer impoundments. Distribution of wildlife among sub-watersheds is given in Table 3.12.

**Table 3.11. Wildlife habitat description and acreage, and percent direct fecal deposition in streams in the Deep Run watershed.**

Wildlife Type	Habitat	Acres of Habitat	Population Density (animal/ac-habitat)	Direct Fecal Deposition in Streams (%)
Deer	Primary: Forest and agricultural areas Secondary: rest of watershed	17,236	0.086 <sup>a,c</sup>	0.1
Raccoon	Primary: 600 feet buffer around streams and impoundments Secondary: 601 feet - 7,920 feet buffer from streams and impoundments	17,236	0.07 <sup>c</sup>	0.1
Muskrat	Primary: 66 feet buffer around streams and impoundments in forest and cropland Secondary: 67-300 feet buffer from same	2,505	2 <sup>a, c</sup>	0.25
Beaver	300 feet buffer around streams and impoundments in forest and pasture	4,700	0.015 <sup>c</sup>	0.5
Geese	300 feet buffer around main streams	2,505	0.078 – off season <sup>b</sup> 0.292 – peak season <sup>a,b</sup>	0.25
Wood Duck	300 feet buffer around main streams	2,505	0.0624 – off season <sup>b</sup> 0.0543 – peak season <sup>b</sup>	0.25
Wild Turkey	Entire watershed except urban areas	17,185	0.01 <sup>c</sup>	0

<sup>a</sup> Original wildlife population densities acquired from VDGIF, USF&WS and published values and adjusted to reflect TAC feedback.

<sup>b</sup> Waterfowl densities obtained from USF&WS biologists.

<sup>c</sup> Species densities obtained from VDGIF biologists.

**Table 3.12. Distribution of wildlife among sub-watersheds in Deep Run watershed.**

Subwatershed	Deer	Raccoon	Muskrat	Beaver	Geese	Wood Duck	Wild Turkey
D-1	216	176	738	11	106	20	25
D-2	163	132	600	4	80	15	19
D-3	196	159	658	10	96	18	23
D-4	189	154	518	8	94	17	22
D-5	216	176	558	6	106	20	25
D-6	184	150	752	8	92	17	21
D-7	251	205	988	9	124	23	29
D-8	69	56	198	2	34	6	8
<b>Total</b>	<b>1,484</b>	<b>1,208</b>	<b>5,010</b>	<b>58</b>	<b>732</b>	<b>136</b>	<b>172</b>

### 3.5 Summary: Contribution from All Sources

A synopsis of the fecal coliform loads characterized and accounted for in the Deep Run watershed along with average fecal coliform production rates are shown in Table 3.13. The total fecal coliform production by all sources in the Deep Run watershed is  $7.25 \times 10^{15}$  cfu/yr.

**Table 3.13. Potential fecal coliform sources and daily fecal coliform production by source in Deep Run watershed.**

Potential Source	Population in Watershed	Fecal Coliform Produced ( $\times 10^6$ cfu/AU-day) <sup>a</sup>	Fecal Coliform Produced ( $\times 10^8$ cfu/ day) <sup>b</sup>
Dairy Cattle			
<i>Milk and Dry Cows</i>	175	25,000	43,750
<i>Heifers</i>	125	8,800	11,000
Beef Cattle (pairs)	263	33,000	88,400
Horses	286	420	1,200
Sheep	15	12,000	10,300
Goats	55	28,000	11,800
Humans	2,524	1,950	49,200
Pets	1,966	450	8,847
Deer	1,484	350	5,194
Raccoon	1,208	50	604
Muskrat	5,010	25	1,253
Beaver	58	0.2	0.12
Wild Turkey	172	93	160
Duck	136	2,400	3,264
Goose	732	800	5,856

<sup>a</sup>Source: Keeling (2003) - Production per animal unit per species.

<sup>b</sup>Fecal coliform production adjusted to account for local animal weight. This may not equal the product of the other two columns.

Based on the inventory of fecal coliform sources, a summary of the contributions made by the nonpoint sources to annual fecal coliform loading directly to the stream and to various land use categories is given in Table 3.14. Distribution of annual fecal coliform loading from nonpoint sources among the different land use categories is also given in Table 3.14.

From Table 3.14, it is clear that nonpoint source loadings to the land surface are more than 240 times larger than direct loadings to the streams, with pastures receiving about 83% of the total fecal coliform load. It could be prematurely assumed that most of the fecal coliform loading in streams originates from upland sources, primarily from pastures. However, other factors such as precipitation (amount and pattern), manure application activities (time and method), type of waste (solid versus liquid manure), proximity to streams and environmental factors also impact the amount of fecal coliform from upland areas that reaches the stream. The HSPF model considers these factors when estimating fecal coliform loads to the receiving waters, as described in Chapter 4.

**Table 3.14. Annual fecal coliform loadings to the stream and the various land use categories in the Deep Run watershed.**

<b>Source</b>	<b>Fecal Coliform Loading (<math>\times 10^{13}</math> cfu/year)</b>	<b>Percent of Total Loading</b>
<i>Direct Loading to Streams</i>		
Straight Pipes	2.270	0.37%
Cattle in Stream	0.197	0.03%
Wildlife in Stream	7.760	1.26%
<i>Loading to Land Surfaces</i>		
Cropland	8.9	1.45%
Pasture 1	370.0	60.25%
Pasture 2	114.0	18.57%
Pasture 3	22.6	3.68%
Forest	19.5	3.18%
Residential	68.8	11.21%
<b>Total</b>	<b>614.0</b>	<b>100.00%</b>

\*Includes loads received from failed septic systems and pets.



## **Chapter 4. Modeling Process for Fecal Coliform TMDL Development**

A key component in developing a TMDL is establishing the relationship between pollutant loadings (both point and nonpoint) and in-stream water quality conditions. Once this relationship has been developed, management options for reducing pollutant loadings to streams can be assessed. In developing a TMDL, it is critical to understand the processes that affect the fate and transport of the pollutants and cause the impairment of the water body of concern. Pollutant transport to water bodies is evaluated using a variety of tools, including monitoring, geographic information systems (GIS), and computer simulation models. In this chapter, modeling process, input data requirements, model calibration procedure and results, and model validation results are discussed.

### **4.1 Model Description**

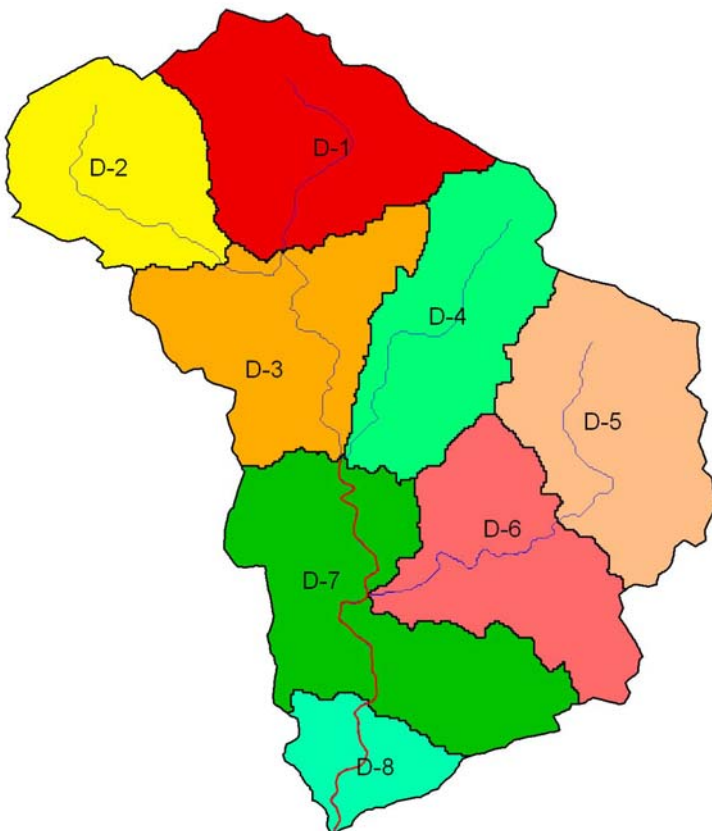
Conducting a TMDL study requires the use of a watershed-based model that integrates both point and nonpoint sources and simulates in-stream water quality processes. The HSPF (Bicknell et al., 2000) was used to model fecal coliform transport and fate in the Deep Run watershed. The ArcView 3.2 GIS program was used to display and analyze landscape information.

The HSPF model simulates nonpoint source runoff and pollutant loadings, performs flow routing through streams, and simulates in-stream water quality processes (Bicknell et al., 2000). HSPF estimates runoff from both pervious and impervious parts of the watershed and stream flow in the channel network. The sub-module PWATER within the module PERLND simulates runoff, and hence, estimates the water budget on pervious areas (e.g., agricultural land). Runoff from largely impervious areas is modeled using the IWATER sub-module within the IMPLND module. The simulation of flow through the stream network is performed using the sub-modules HYDR and ADCALC within the module RCHRES. While HYDR routes the water through the stream network, ADCALC calculates variables used for simulating convective transport of the pollutant in the stream. Fate of fecal coliform on pervious and impervious land segments is simulated using the PQUAL (PERLND module) and IQUAL (IMPLND module) sub-modules, respectively. Fate of fecal coliform in stream water is simulated using the GQUAL sub-module within RCHRES module. Fecal coliform bacteria are simulated as a dissolved pollutant using the general constituent pollutant model (GQUAL) in HSPF.

The HSPF model requires a wide variety of input data to describe hydrology, water quality, and land use characteristics of the watershed. The different types and sources of input data used to develop the model for the Deep Run watershed are discussed below in Sections 4.2 through 4.6. This information is translated into model parameters. Hydrology parameters required for the PWATER, IWATER, HYDR, and ADCALC sub-modules are listed in BASINS Version 3.0 User's Manual 3.0 (USEPA, 2001). Water quality parameters required as inputs for PQUAL, IQUAL, and GQUAL are given in the BASINS Version 3.0 User's Manual (USEPA, 2001). Values for the hydrology and water quality parameters were estimated based on local conditions when possible; otherwise the default parameters provided within HSPF were used.

## 4.2 Selection of Sub-watersheds

Deep Run is a moderately sized watershed (17,283 acres) and the model framework selected is suitable for this size. To account for the spatial distribution of fecal coliform sources, the watershed was divided into eight subwatersheds as shown in Figure 4.1. Tributaries to the impaired segment of Deep Run (D-7,8) include an unimpaired segment of Deep Run (D-1,3), Green Branch (D-4), Alcott Run (D-5,6), and an unnamed tributary (D-2). The stream network was delineated based on the blue line stream network from USGS topographic maps with each subwatershed having at least one stream segment. Subwatershed delineation was based on potential fecal loadings, flow and water quality data availability, and HSPF model constraints. Because loadings of fecal coliform are believed to be associated with land use activities, subwatersheds were chosen based on uniformity of land use. HSPF outputs flow and fecal coliform concentration at subwatershed outlets, therefore subwatershed outlets were chosen to correspond to flow and water quality station locations. An hourly model time-step was used requiring the time of concentration in each subwatershed to be greater than one hour.



**Figure 4.1. Deep Run subwatersheds.**

### 4.3 Land Use

The National Land Cover Data (NLCD) produced by U.S. Geological Survey (USGS) in cooperation with the USEPA was used for this study. NLCD was developed from 30-meter Landsat thematic mapper (TM) data between 1990 and 1994 acquired by the Multi-resolution Land Characterization (MRLC) Consortium, a partnership between USGS, USEPA, U.S. Forest Service, and National Oceanic and Atmospheric Administration. NLCD is classified into 21 land use types. The NLCD land use types within the watershed were consolidated into eight categories based on similarities in hydrologic and waste application/production features (Table 4.1). The land use categories were assigned pervious/impervious percentages, which allowed a land use with both pervious and impervious fractions to be modeled using both the PERLND and IMPLND modules. Some hydrology and water quality model parameters used in the PERLND and IMPLND modules are a function of land use.

**Table 4.1. Consolidation of NLCD land use categories for Deep Run watershed.**

<b>TMDL Land Use Categories</b>	<b>Pervious / Impervious* (%)</b>	<b>NLCD Land use Classification (Class No.)</b>
Cropland	Pervious (100)	Row Crops (82) Small grains (83)
Pasture 1	Pervious (100)	Pasture/Hay (81)
Pasture 2	Pervious (100)	Pasture/Hay (81)
Pasture 3	Pervious (100)	Pasture/Hay (81)
Urban	Pervious (80), Impervious (20)	Commercial/Industrial/Transportation (23)
Residential	Pervious (80), Impervious (20)	Low Density Residential (21) High Intensity Residential (22)
Forest	Pervious (100)	Transitional (33) Deciduous Forest (41) Evergreen Forest (42) Mixed Forest (43) Woody Wetlands (91) Emergent Herbaceous Wetlands (92)
Water	Impervious (100)	Open Water (11)

\*Percent pervious / impervious information was used in modeling (described in later sections).

As discussed in Section 4.2, eight subwatersheds were defined to spatially analyze waste or fecal coliform distribution within the watershed (Figure 4.1). Land use distribution in the subwatersheds as well as in the entire Deep Run watershed is presented in Table 4.2.

**Table 4.2. Land use distribution in Deep Run watershed (acres).**

Subshed	Land Use (ac)							
	Cropland	Pasture1	Pasture2	Pasture3	Urban	Residential	Forest	Total
D-1	241.0	211.6	106.0	53.0	5.5	35.9	1,856.0	2,509.0
D-2	83.6	78.1	39.1	19.6	2.3	16.3	1,651.3	1,890.2
D-3	118.3	124.9	62.5	31.3	0.5	24.0	1,937.8	2,275.3
D-4	168.0	162.5	81.4	40.7	0.7	22.0	1,739.7	2,193.0
D-5	260.7	252.1	126.3	63.1	1.8	12.4	1,790.6	2,507.1
D-6	147.7	145.1	72.7	36.3	0.0	5.6	1,736.0	2,143.4
D-7	311.8	301.5	151.0	75.5	1.4	49.2	2,031.8	2,922.2
D-8	34.0	36.6	18.3	9.2	0.0	2.9	695.6	796.5
<b>Total</b>	<b>1,365.2</b>	<b>1,312.4</b>	<b>657.3</b>	<b>328.7</b>	<b>12.1</b>	<b>168.3</b>	<b>13,438.8</b>	<b>17,282.7</b>

#### 4.4 Stream Channel Characteristics

For each stream reach, a function table (F-Table) is required to describe the relationship between water depth, surface area, volume, and discharge (Bicknell et al., 2000). These parameters were estimated by surveying representative channel cross-sections in each subwatershed. Trapezoidal channel geometry with pitch breaks at the beginning of the flood plain was developed for each reach. Information on stream geometry in each subwatershed is presented in Table 4.3.

**Table 4.3. Stream Channel Characteristics Used to Calculate F-Tables in the Deep Run Watershed.**

Sub-shed	Stream Length (mile)	Average Width (ft)	Average Depth (ft)	Stream Relief (ft/ft)	Channel Slope (ft/ft)	Channel Manning's n <sup>a</sup>	Flood Plain Manning's n <sup>a</sup>
D-1	2.40	4.25	1.75	0.0065	1.50	0.060	0.085
D-2	2.65	4.75	2.00	0.0068	1.75	0.060	0.085
D-3	3.37	9.00	3.00	0.0064	1.25	0.053	0.070
D-4	3.48	5.00	2.00	0.0059	1.75	0.055	0.078
D-5	2.51	4.25	3.50	0.0054	2.25	0.055	0.085
D-6	2.48	12.00	5.25	0.0068	1.75	0.050	0.075
D-7	3.26	16.00	4.50	0.0063	0.95	0.050	0.063
D-8	1.66	25.00	9.00	0.0037	1.08	0.050	0.065

<sup>a</sup> Dimensionless.

#### 4.5 Climatological Data

The climate data needed for model simulations conducted as a part of this study were obtained from the National Climatic Data Center (NCDC) (NCDC, 2003), part of the National Weather Service (NWS). Hourly weather data needed to conduct model simulations in the paired watershed, Battle Run, were taken from the Piedmont Research Station (446712) weather station (paired watershed discussed in Section 4.8). Simulations performed for Deep Run used hourly weather data from the Culpeper (442159) weather station. Daily precipitation was transformed to address discrepancies (i.e., missing data) between observed runoff and hourly precipitation records. Using hourly precipitation data, frequency of precipitation events and precipitation amounts per hour were calculated. For daily precipitation amounts equal to or

less than 0.3 inches, the daily amount was assigned to the hour with the highest likelihood of rainfall. For daily rainfall amounts greater than 0.3 inches, the daily amount was distributed over the day using the calculated hourly precipitation amount frequency distribution.

## 4.6 Accounting for Pollutant Sources

### 4.6.1 Overview

Currently, no VPDES or MS4 permitted facilities exist in the Deep Run watershed. No fecal coliform load was modeled originating from permitted point facilities.

Fecal coliform loads that are directly deposited by straight pipes and cattle along with wildlife in streams were treated as direct nonpoint sources in the model. Fecal coliform that is land-applied or deposited on land was treated as nonpoint source loading; all or part of that load may get transported to the stream as a result of surface runoff during rainfall events. Direct nonpoint source loading was applied to the stream in each sub-watershed as appropriate.

Nonpoint source loading was applied as fecal coliform counts to the pervious fraction of each land use category in a sub-watershed on a daily basis. Both direct nonpoint and nonpoint source loadings were varied by month to account for seasonal differences such as cattle and wildlife access to streams. Nonpoint source loading was applied as fecal coliform counts to the impervious fraction of each land use category in a subwatershed at a constant rate during the year. These constant application rates are a function of land use and are discussed in detail in Section 4.6.4. Fecal coliform die-off was simulated during periods when manure is stored, while on the land between runoff generating precipitation events, and while in streams.

### 4.6.2 Modeling Fecal Coliform Die-off

Fecal coliform die-off was modeled using a first order die-off equation of the form:

$$C_t = C_0 10^{-kt} \quad [4.1]$$

where:  $C_t$  = concentration or load at time  $t$ ;

$C_0$  = starting concentration or load (cfu/ 100ml);

$K$  = decay rate (day<sup>-1</sup>); and

$t$  = time in days.

A review of literature provided estimates of decay rates that could be applied to waste storage and handling in the Deep Run watershed (Table 4.4).

**Table 4.4. First order decay rates for different animal waste storage as affected by storage/application conditions and their sources in the Deep Run watershed.**

Waste Type	Storage / Application	Decay Rate (1/day)	Reference
Dairy Manure	Pile (not covered)	0.066	Jones (1971)*
	Pile (covered)	0.028	
Beef Manure	Anaerobic Lagoon	0.375	Coles (1973)*

\*Cited in Crane and Moore (1986).

Based on the values cited in the literature, the following decay rates were used in simulating fecal coliform die-off in stored waste.

- Liquid dairy manure: no decay rate for liquid dairy manure storage could be found in the literature, therefore the decay rate for beef manure in anaerobic lagoons (0.375 / day) was used.
- Solid cattle manure: based on the range of decay rates (0.028-0.066 / day) reported for solid dairy manure, a decay rate of 0.05 / day was used assuming that a majority of manure piles are not covered.

Based on these decay rates, die-off of fecal coliform in different storage capacities at the end of the respective storage period were calculated using Equation [4.1]. Depending on the duration of storage, type of storage, type of manure, and die-off factor, the fraction of fecal coliform surviving in the manure at the end of storage was calculated. While calculating survival fraction at the end of the storage period, the daily addition of manure and coliform die-off of each fresh manure addition was considered to arrive at an effective survival fraction over the entire storage period. By multiplying the survival fraction with total fecal coliform produced per year (in as-excreted manure), the amount of fecal coliform available for application to land per year was estimated. Monthly fecal coliform application to land was estimated by multiplying the amount of fecal coliform available for application to land per year by the fraction of manure applied to land during that month. The decay rate for fecal coliform on the land surface was represented in HSPF by specifying a maximum surface buildup (i.e., MON-SQOLIM) based on the daily loading rate (i.e., MON-ACCUM). An in-stream decay rate for each reach segment (i.e., FSTDEC) was specified in HSPF.

#### **4.6.3 Modeling Direct Nonpoint Sources**

Fecal coliform loads from direct nonpoint sources included straight pipes, cattle in streams, and wildlife in streams. Also, contribution of fecal coliform from interflow was modeled as having a constant concentration of 4 cfu/100mL. Based on TAC feedback, no instances of groundwater contamination were acknowledged and as a result it was assumed that the groundwater contained no bacteria. Loads from direct nonpoint sources in each watershed are described in detail in Chapter 3.

#### **4.6.4 Modeling Land-based Nonpoint Sources**

For modeling purposes, nonpoint fecal coliform loads were those that were deposited or applied to land and, hence, required surface runoff events for transport to streams. Fecal coliform loading by land use for all sources in each sub-watershed is presented in Chapter 3. The existing condition fecal coliform loads are based on best estimates of existing wildlife, livestock, human, and pet populations along with fecal coliform production rates. Fecal coliform in stored waste was adjusted for die-off prior to the time of land application when calculating loadings to cropland and pasture. For a given period of storage, the total amount of fecal coliform present in the stored manure was adjusted for die-off on a daily basis. The sources of

fecal coliform to different land use categories and how the model handled them are briefly discussed below.

- Cropland: Where applicable liquid dairy manure and solid manure are applied to cropland as described in Chapter 3. Fecal coliform loadings to cropland were adjusted to account for die-off during storage and partial incorporation during land-application. Wildlife contributions were also added to the cropland areas. For modeling, monthly fecal coliform loading assigned to cropland was distributed over as many acres within the subwatershed as were needed to utilize the generated manure. Thus, loading rate varied by month and sub-watershed.
- Pasture: The only deposition of manure on pasture resulted from deposition from livestock and wildlife as described in Chapter 3. For modeling, the monthly fecal coliform loading assigned to pasture was distributed over the entire pasture acreage within a sub-watershed. Thus, loading rate varied by month and sub-watershed.
- Residential: Fecal coliform loading on the pervious fraction of this land use category is described in Chapter 3. Residential land use loading came from failing septic systems, wildlife, and waste from pets. In the model simulations, fecal coliform loads produced by failing septic systems and pets in a sub-watershed were combined and assumed to be uniformly applied. Loading to the impervious fraction of this land use category was assumed constant throughout the year varying per subwatershed.
- Urban: This land use category was comprised chiefly of the commercial/industrial/transportation areas. Fecal coliform loadings on the pervious fraction of this land use were allowed to vary monthly. Loading to the impervious fraction of this land use category was assumed to be constant throughout the year varying per subwatershed. Source categories contributing to this land use include pets.
- Forest: Wildlife not defecating in streams or on cropland and pastures provided fecal coliform loading to the forested land use. Fecal coliform from wildlife was applied uniformly over the forest areas, except for the percentage considered as direct load to forested streams.

#### **4.6.5 Modeling Existing BMPs**

Data describing existing best management practices (BMPs) were provided by staff from the Virginia Department of Conservation and Recreation, Virginia Cooperative Extension, Soil and Water Conservation Districts, and agricultural producers. Additional data were collected during windshield surveys in the watershed. These data were applied in multiple fashions when developing the model to represent the effects of BMPs on loads and load transport. BMPs were either accounted for directly in the development of loads associated with direct deposition and/or deposition on specific land uses, accounted for during calibration of the water quality model, or incorporated into the implicit margin of safety (MOS).

BMPs incorporated directly into the model, such as collection, storage, and spreading of confined animal waste were modeled as previously described. Die-off during storage was

accounted for prior to spreading, as well as after spreading. Three grades of pasture were modeled to represent pasture management practices observed in the watershed. Reductions in stream access based on exclusion fencing were accounted for directly when developing the cattle distribution schedules in Tables 3.6 and 3.7.

Due to a shortage of data describing bacteria removal efficiencies, some BMPs were accounted for during calibration. Grassed buffer strips between pasture or crop and stream edges is a good example of an identified BMP that was accounted for during calibration of the water quality model.

Identified BMPs that were not directly accounted for during load development or model calibration were incorporated into the implicit MOS. The MOS accounts for uncertainty in the model and helps ensure that the final TMDL allocation will enable the stream to meet water quality standards when implemented.

## **4.7 Model Calibration and Validation**

Model calibration is the process of selecting model parameters that provide an accurate representation of the watershed. Validation ensures that the calibrated parameters are appropriate for periods other than the calibration period. In this section, the procedures followed for calibrating the hydrology and water quality components of the HSPF model are discussed. The calibration and validation results of the hydrology and water quality components are presented.

### **4.7.1 Hydrology**

Observed stream flow values were not available for Deep Run, therefore a “paired watershed” approach was used for hydrologic calibration and validation. The approach assumes that the paired watershed and Deep Run watershed have similar hydrologic responses based on physical, geologic, and hydrologic characteristics. Five parameters were compared between the Deep Run and potential paired watersheds with long-term USGS flow-monitoring data: size, land use distribution, slope, prominent soil hydrologic group, and geology. The Battle Run watershed was chosen as the paired watershed due to similar physiographic and hydrologic characteristics (Table 4.5). Hydrology calibration and validation were performed based on the physical, hydrologic, and land use data for the Battle Run watershed. After calibration and validation completion, the parameterization for the Battle Run model was transferred to the Deep Run model. Parameters describing watershed characteristics such as land use, slope, infiltration rate, and F-Tables were updated to reflect the physical properties in Deep Run.



**Table 4.5. Summary of the Physical Properties of the Deep Run and Battle Run watersheds.**

Physical Characteristic	Deep Run Watershed	Battle Run Watershed
Size (mi <sup>2</sup> )	27	26
<i>Land Use (%)</i> :		
Forest	78	46
Pasture/Cropland	20	53
Urban/Residential	1	1
Slope (ft/ft)	0.0061	0.0084
Prominent Soil Hydrologic Groups	C/D	B/D
Geology	Piedmont	Blue Ridge

The Battle Run model was calibrated using observed flow values from USGS station at Battle Run near Laurel Mills, VA (#01662800) for the period March 1, 1981 to June 15, 1985 (USGS, 2003). The model was validated for the period January 1, 1990 to June 30, 1993. The daily average flow data were used in the hydrologic calibration and validation. Output from the HSPF model for both calibration and validation was daily average flow in cubic feet per second (cfs). Calibration parameters were adjusted within the recommended ranges until the model performance was deemed acceptable.

The HSPEXP decision support system developed by USGS and tools developed by Engineering Concepts, Inc. were used to calibrate and validate the hydrologic portion of HSPF. Calibration and validation criteria as well as model performance are presented in Table 4.6 and 4.7, respectively. All criteria were within the recommended ranges. As shown in Figures 4.2 and 4.3, the simulated flow for both the calibration and validation matched the observed flow well. The agreement with observed flows is further illustrated in Figures 4.4 and 4.5 for a representative year and Figures 4.6 and 4.7 for a representative storm. The agreement of the simulated and observed time series can be further seen through the comparison of their cumulative frequency curves (Figures 4.8 and 4.9).

**Table 4.6. Summary statistics for the calibration period (3/1/81 to 6/15/85) in Battle Run watershed.**

	<b>Criterion</b>	<b>Observed</b>	<b>Modeled</b>	<b>Error (%)</b>
Total Runoff (in)	10%	58.82	61.44	4.45
Total of Highest 10% Flows (in)	15%	27.78	26.36	-5.10
Total of Lowest 50% Flows (in)	10%	7.93	7.77	-1.95
Total Winter Runoff (in)	20%	23.22	24.95	7.46
Total Summer Runoff (in)	20%	4.16	4.63	11.37
Total Storm Runoff (in)	20%	56.92	57.53	1.08
Groundwater Recession Coefficient	1%	0.94	0.95	1.0
Coefficient of Determination, $r^2$	0.68			

**Table 4.7. Summary statistics for the validation period (1/1/90 to 6/30/93) in Battle Run watershed.**

	<b>Criterion</b>	<b>Observed</b>	<b>Modeled</b>	<b>Error (%)</b>
Total Volume (in)	10%	58.11	59.67	2.69
Total of Highest 10% Flows (in)	15%	24.50	23.15	-5.49
Total of Lowest 50% Flows (in)	10%	9.03	9.13	1.06
Total Winter Flow (in)	20%	23.18	26.01	12.19
Total Summer Flow Volume (in)	20%	3.67	3.24	-11.65
Total Storm Volume (in)	20%	57.02	56.89	-0.23
Groundwater Recession Coefficient	1%	0.94	0.95	1.0
Coefficient of Determination, $r^2$	0.61			

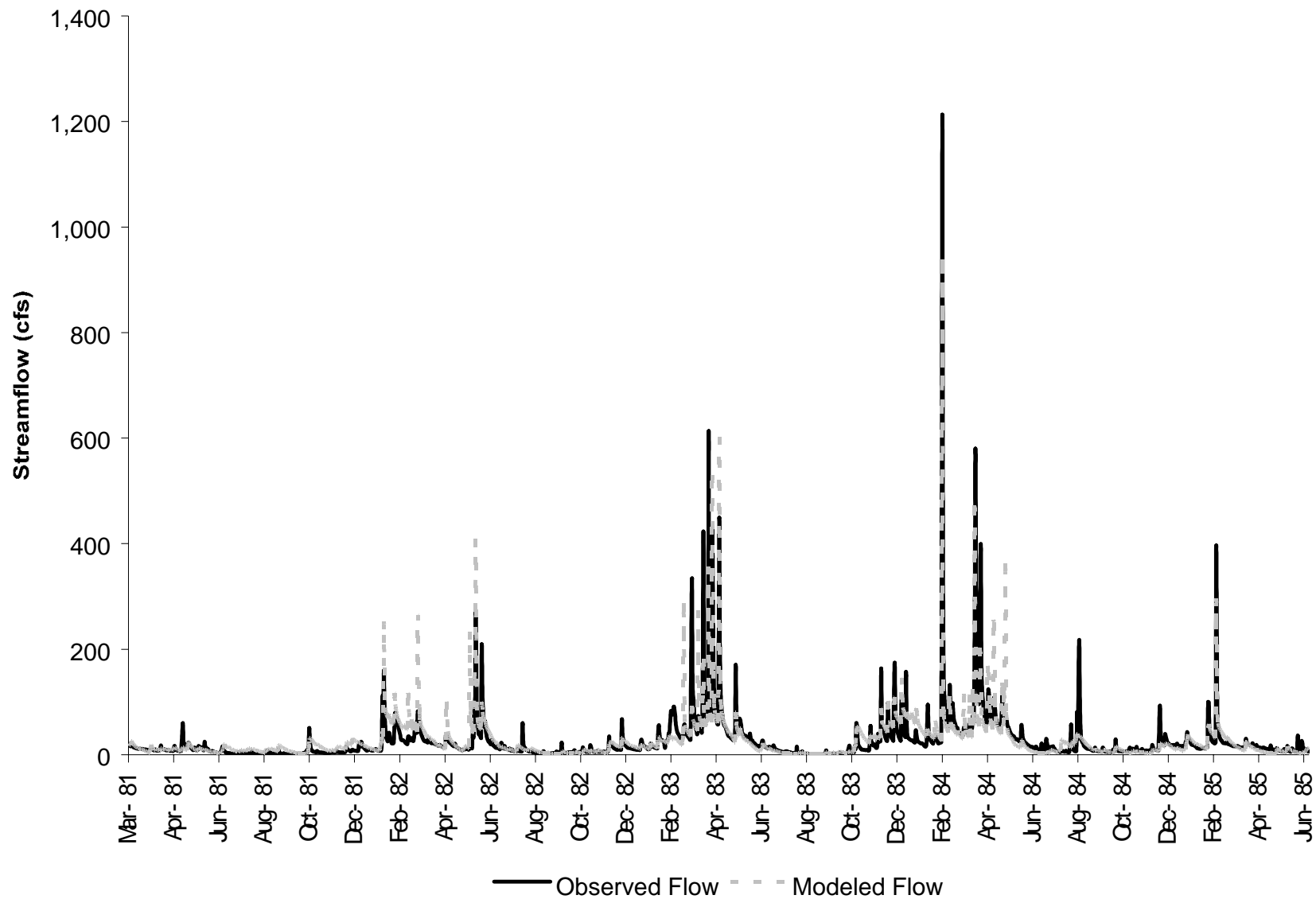


Figure 4.2. Observed and modeled flows for the calibration period 3/1/81 to 6/15/85 in Battle Run watershed.

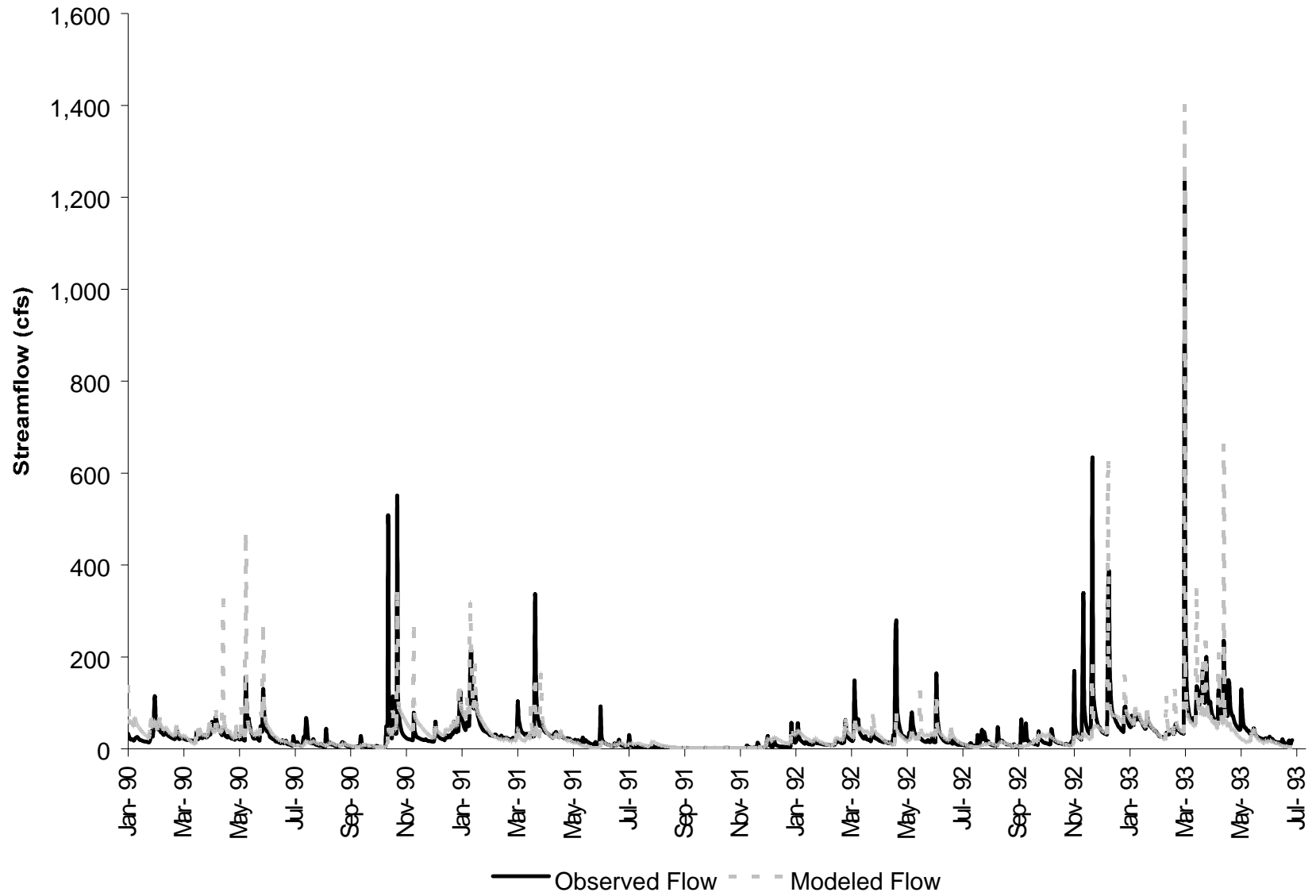
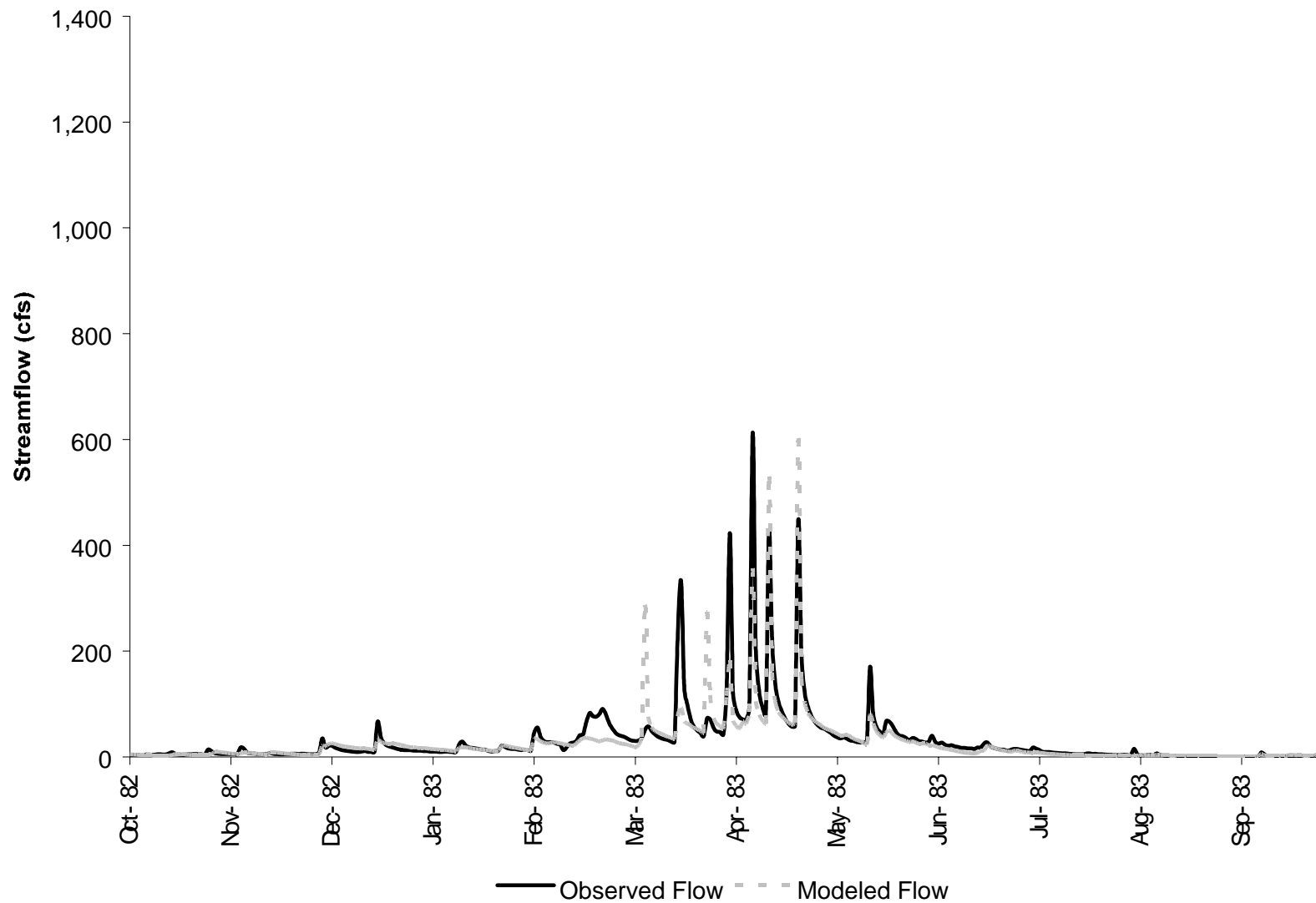
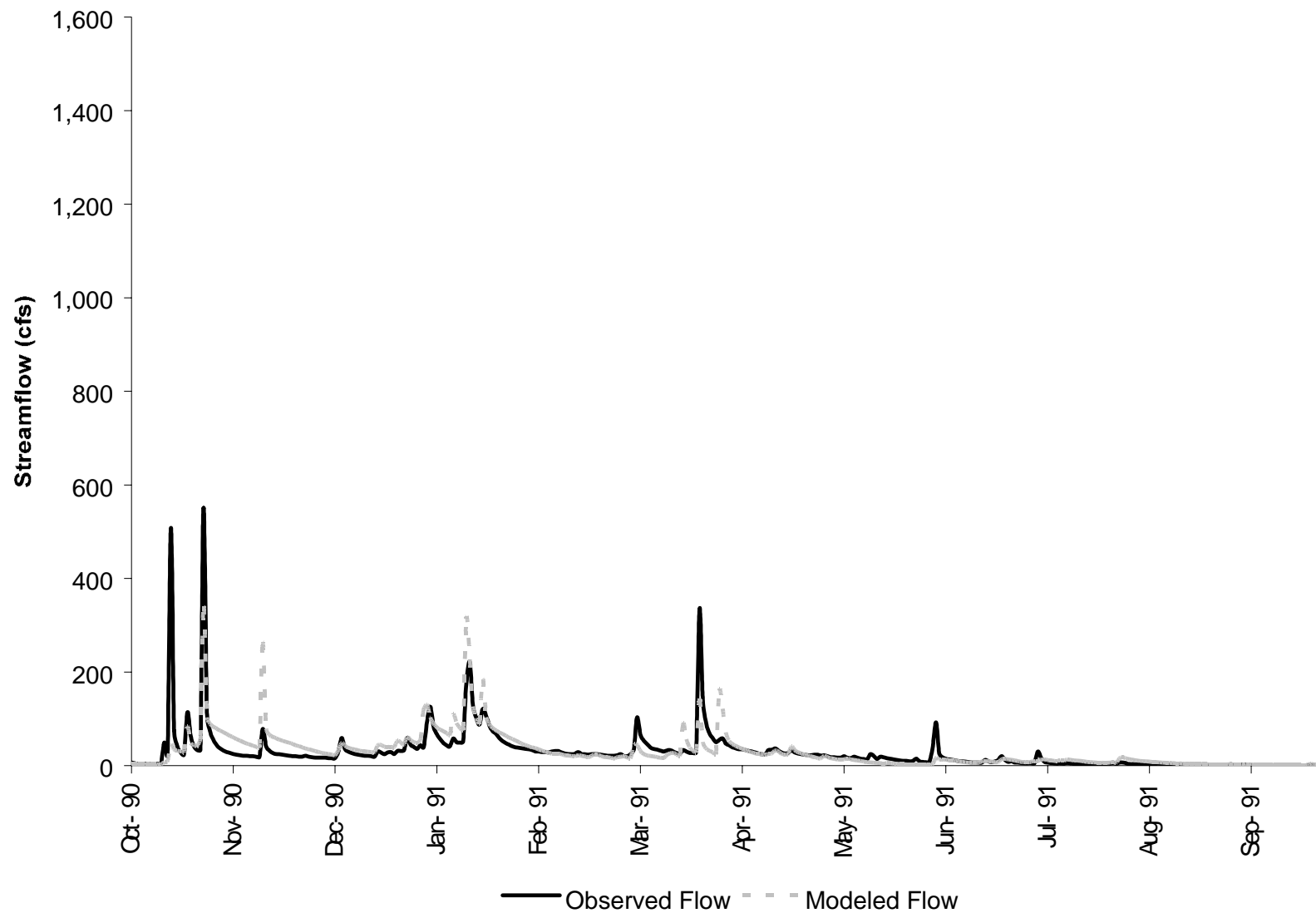


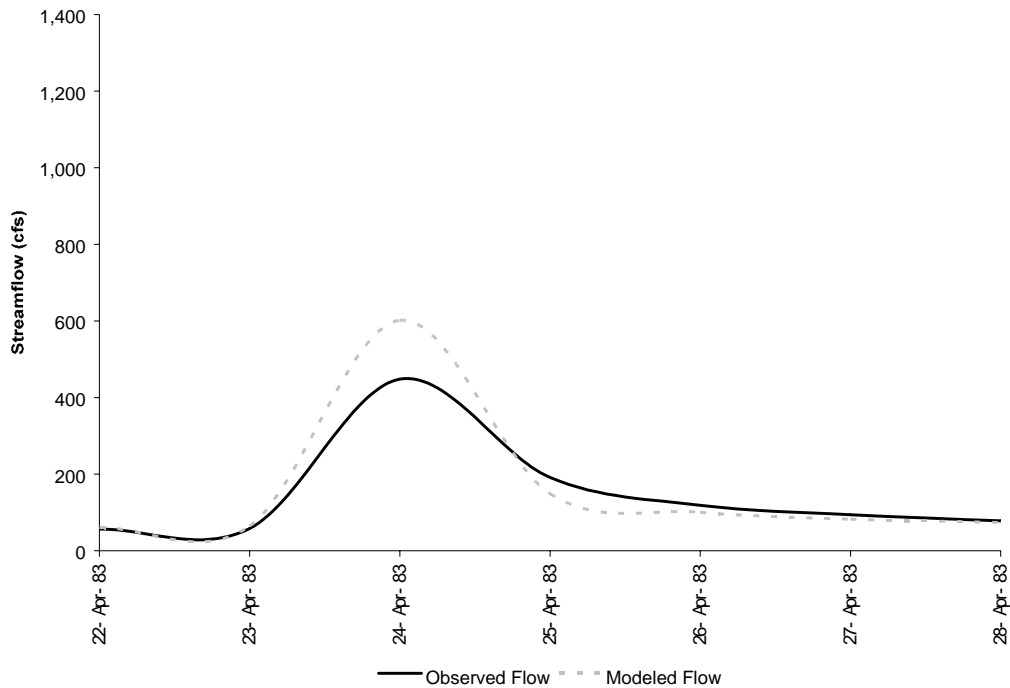
Figure 4.3. Observed and modeled flows for the validation period 1/1/90 to 6/30/93 in Battle Run watershed.



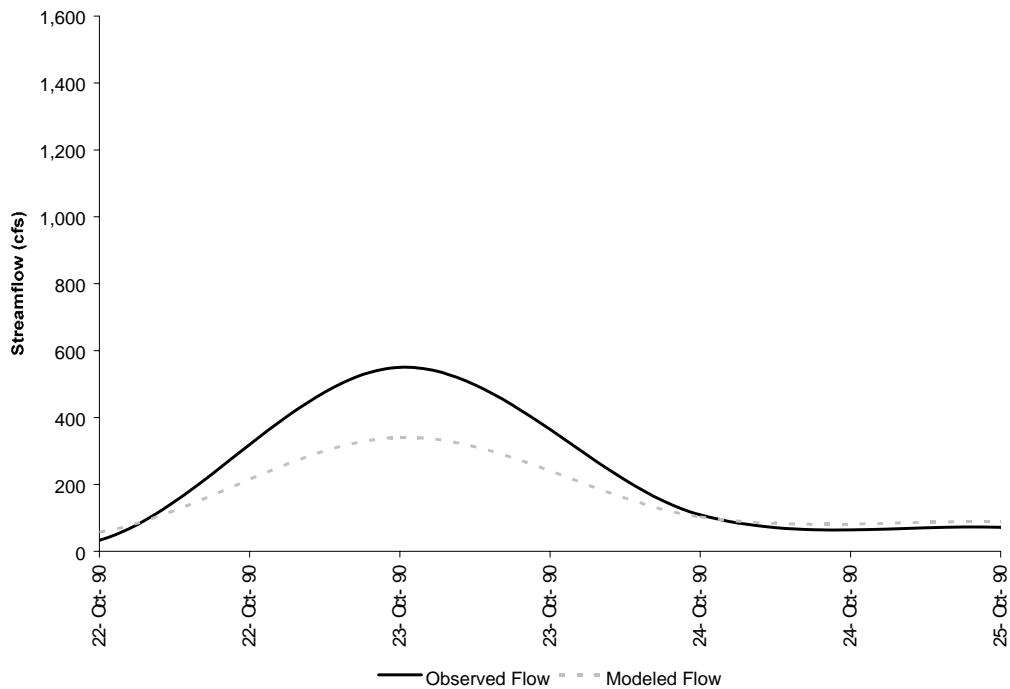
**Figure 4.4. Observed and modeled flows for a representative water year (10/1/82 to 9/30/83) during the calibration period Battle Run watershed.**



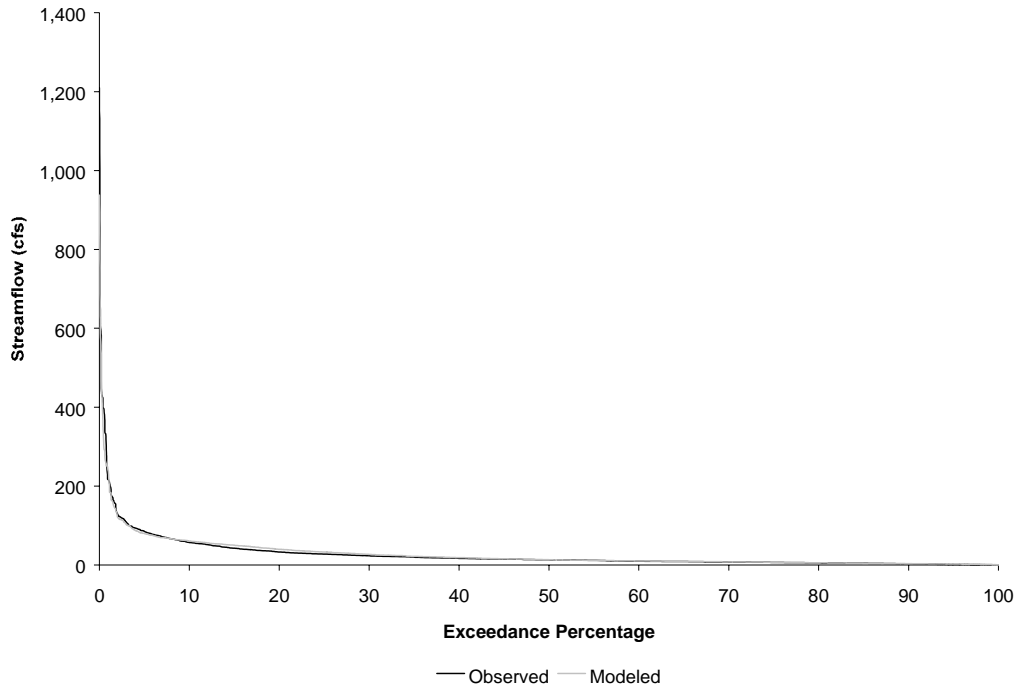
**Figure 4.5. Observed and modeled flows for a representative water year (10/1/90 to 9/30/91) during the validation period in Battle Run watershed.**



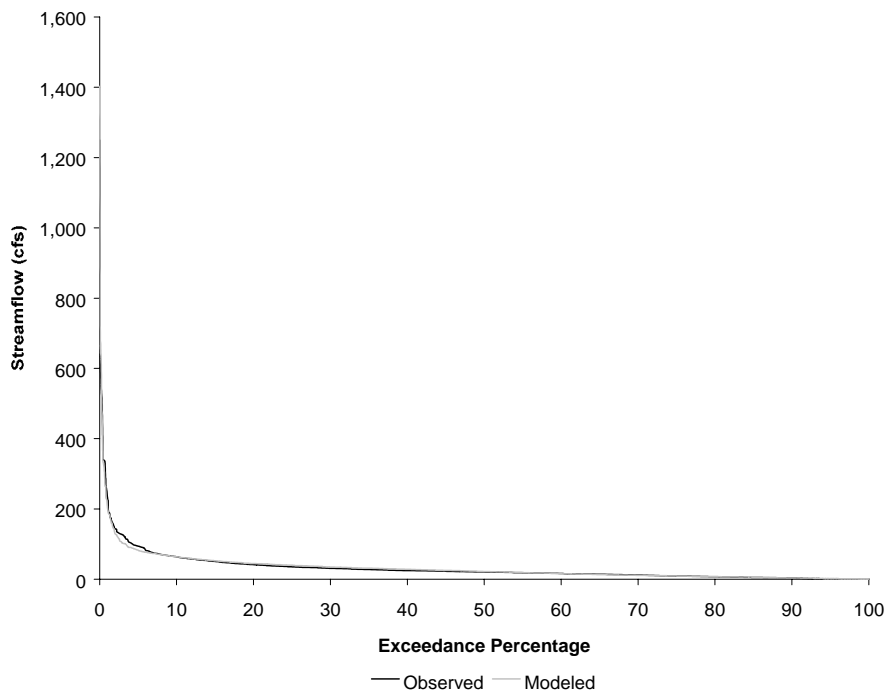
**Figure 4.6. Observed and modeled flows for a representative storm (4/23/83-4/30/83) during the calibration period in Battle Run watershed.**



**Figure 4.7. Observed and modeled flows for a representative storm (1/9/91-1/15/91) during the validation period in Battle Run watershed.**



**Figure 4.8. Cumulative frequency curves for the calibration period 3/1/81 to 6/15/85 in Battle Run watershed.**



**Figure 4.9. Cumulative frequency curves for the validation period 1/1/90 to 6/30/93 in Battle Run watershed.**



Flow partitioning for Battle Run and Deep Run hydrologic model calibration and validation is shown in Table 4.8.

**Table 4.8. Flow partitioning for the calibration and validation periods in Battle Run and Deep Run watersheds.**

Average Annual Flow	Battle Run		Deep Run	
	Calibration	Validation	Calibration	Validation
Total Runoff (in)	69.2	60.0	70.7	50.9
Surface Runoff (in)	9.7 (14%)	8.8 (15%)	7.8 (11%)	5.2 (10%)
Interflow (in)	5.4 (8%)	5.0 (8%)	5.7 (8%)	3.9 (8%)
Baseflow (in)	54.1 (78%)	46.2 (77%)	57.2 (81%)	41.8 (82%)

A list of final calibration parameters for the hydrology calibration can be found in the next section (Table 4.9).

#### **4.7.2 Water Quality**

The simulation of water quality concentrations (e.g., bacteria concentrations) is built on the hydrology simulation. The simulation runs at an hourly time step with average daily fecal coliform bacteria concentrations output at the stream reaches. Based on critical period analysis and availability of data, the period of January 1, 1998 through December 31, 2002 was chosen for water quality calibration and January 1, 1993 through December 31, 1997 for water quality validation.

The PQUAL and IQUAL modules of HSPF were used to represent the build-up, die-off, and wash-off of fecal coliform bacteria from land surfaces. The modules are characterized by the following parameters: 1) Daily accumulation rate of bacteria on the soil surface (ACQOP); 2) Maximum bacteria build-up rate on the soil (SQOLIM); 3) Rate of surface runoff that removes 90% of the accumulated bacteria from the soil surface (WSQOP); and 4) Bacteria concentration in interflow, PQUAL only (IOQC). The GQUAL module in HSPF was used to represent the transport, settling, and die-off of dissolved bacteria in-stream. Settling and die-off were estimated using the first-order decay rate (FSTDEC). Additionally, F-Tables were adjusted to account for additional assimilative capacity in the watershed not represented by channel volumes derived for the reach section. Added assimilation can be achieved through three additional pathways. First, only the main channel of Deep Run and its major tributaries are explicitly represented in HSPF. Stream channels not represented add additional water volume available to dilute fecal coliform loads during low flow conditions and increase channel residence time, which increases settling and die-off of bacteria in transit. Second, dead water that occurs during minimal streamflow can provide added storage. Third, flow in the watershed drains through a multitude of farm ponds. Using GIS, ponds were estimated by separating water in the stream layer from water in the land use layer. Surface area of the ponds was multiplied by an estimated depth of four feet to calculate the total storage volume of all ponds in a subwatershed. To account for the three sources of additional storage, an additional storage volume was added to each line of the F-table. This storage has no effect on the functional

relationship between volume of water stored in the channel and flow in the channel. The final calibration parameters are shown in Table 4.9.

Fecal coliform bacteria observations from the VADEQ ambient water quality monitoring stations 3ALC002.74, 3DPR008.98, 3DPR004.93, and 3DPR001.70 within the Deep Run watershed were used to calibrate the water quality component of HSPF. Data from station 3DPR001.70 were only available during the validation period. It should be noted that each observed bacteria concentration datum represents a “snapshot” resulting from the examination of one grab sample, while the modeled data represent a continuous time series of bacteria concentration. Observations from the VADEQ stations, 3ALC002.74, 3DPR008.98, 3DPR004.93, and 3DPR001.70, were graphically compared to corresponding modeled concentrations at subwatersheds 2, 3, 5, and 7 (Figures 4.10 through 4.14). Modeled fecal coliform concentrations generally agree well with the observed fecal coliform concentrations when displayed. Seasonal variations are exhibited by the modeled concentrations, and most observed concentrations are simulated accurately.

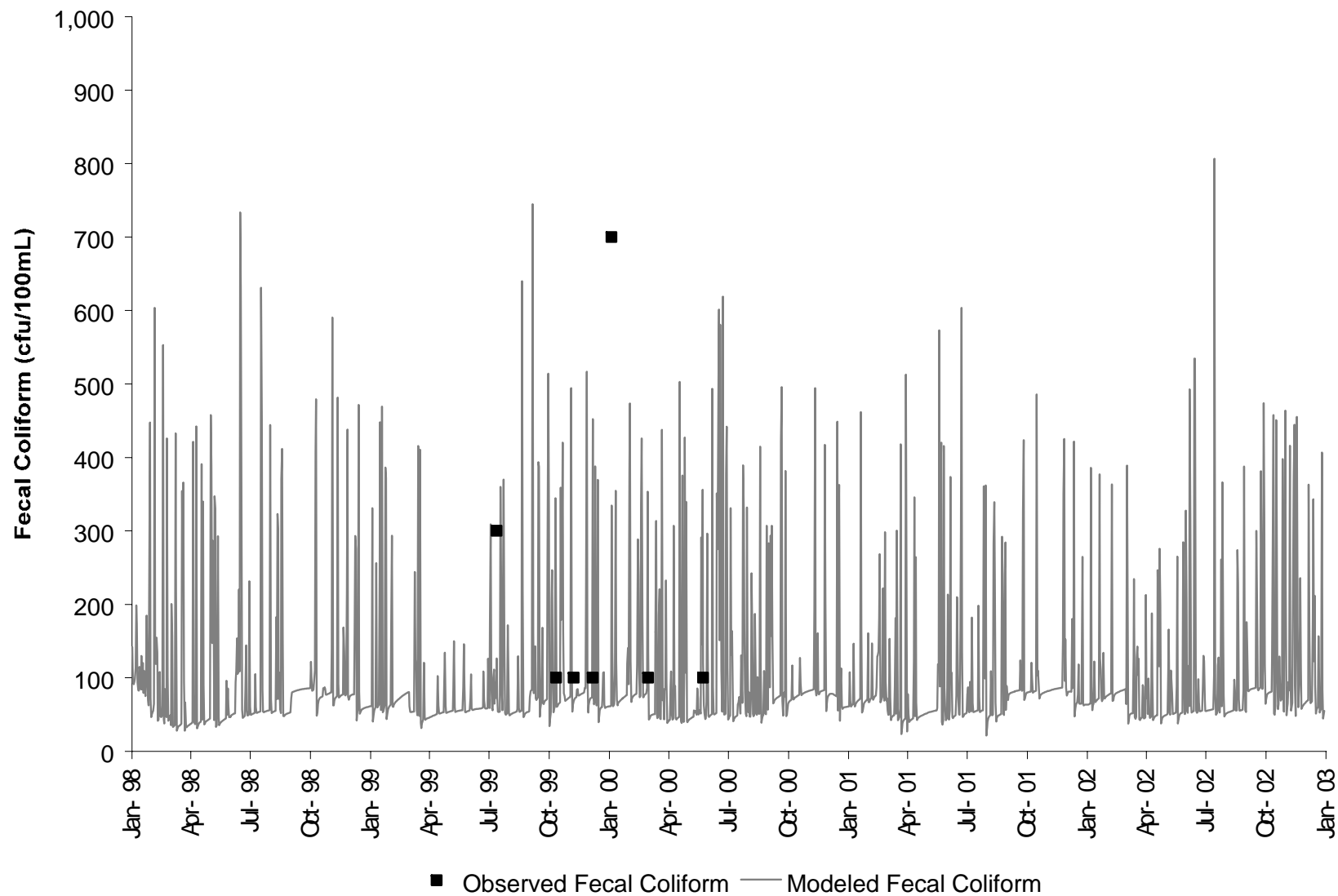
To provide a quantitative measure of the agreement between observed and modeled data, the geometric mean and violation rate of the previous 1,000 cfu/100mL fecal coliform instantaneous standard and the interim 400 cfu/100mL fecal coliform instantaneous standard were calculated. Tables 4.10 and 4.11 show the observed and modeled comparisons of the geometric mean and violation rates for the calibration and validation periods, respectively. It should be noted that a limited number of observed values were available for comparison when determining violation rates in Tables 4.10 and 4.11. A difference of one violation could result in a difference of violation rate of 6-13%. The modeled versus observed geometric mean concentrations and violation rates comparison yielded acceptable results for the calibration period. As seen in Table 4.11, the model underestimated the geometric mean and violation rates for the validation period. Validation results were deemed suitable, however, more emphasis should be placed on the calibration results because there was only one station during validation to compare results and recent changes in the watershed likely affecting bacteria loadings to the stream (e.g., dairy farm closing) are represented in the more current calibration period.

Based on the qualitative and quantitative analyses performed during hydrology and water quality calibration and validation, it was established that the developed model adequately represented the processes and interactions associated with the production and transport of bacteria within the Deep Run watershed.

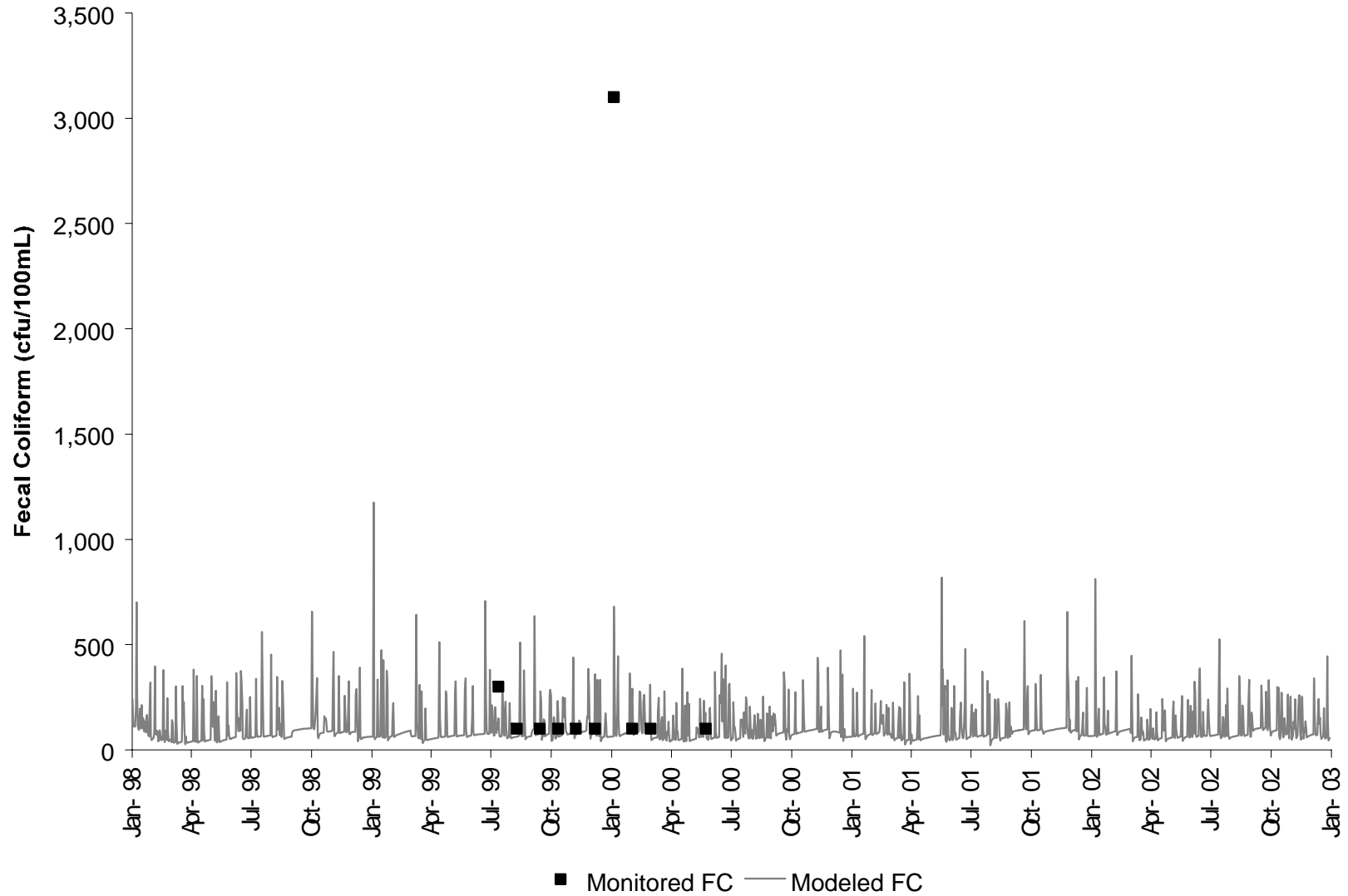
**Table 4.9. Calibrated hydrology and water quality HSPF parameters for Deep Run watershed.**

Parameter	Definition	Units	Range of Values				Start	Final	Function of...
			Typical		Possible				
			Min	Max	Min	Max			
PERLND									
PWAT-PARM2									
FOREST	Fraction forest cover	none	0.00	0.5	0	0.95	0	0–0.5	Forest cover
LZSN	Lower zone nominal soil moisture storage	in	3	8	2	15	2.8	3.5	Soil properties
INFILT	Index to infiltration capacity	in/hr	0.01	0.25	0.001	0.5	0.22	0.19	Soil and cover condition
LSUR	Length of overland flow	ft	200	500	100	700	300	300	Topography
SLSUR	Slope of overland flowplane	none	0.01	0.15	0.001	0.3	0.047	0.047	Determined by GIS
KVARY	Groundwater recession variable	1/in	0	3	0	5	0	0	Calibrate
AGWRC	Base groundwater recession	none	0.92	0.99	0.85	0.999	0.98	0.94	Calibrate
PWAT-PARM3									
PETMAX	Temp below which ET is reduced	deg. F	35	45	32	48	40	40	Climate, vegetation
PETMIN	Temp below which ET is set to zero	deg. F	30	35	30	40	35	35	Climate, vegetation
INFEXP	Exponent in infiltration equation	none	2	2	1	3	2	2	Soil properties
INFILD	Ratio of max/mean infiltration capacities	none	2	2	1	3	2	2	Soil properties
DEEPPFR	Fraction of GW inflow to deep recharge	none	0	0.2	0	0.5	0.3	0.15	Geology
BASETP	Fraction of remain ET from active baseflow	none	0	0.05	0	0.2	0.09	0.056	Riparian vegetation
AGWETP	Fraction of remain ET from active W	none	0	0.05	0	0.2	0	0	Marsh/wetlands ET
PWAT-PARM4									
CEPSC	Interception storage capacity	in	0.03	0.2	0.01	0.4	0.1	0.06-0.20	Vegetation
UZSN	Upper zone nominal soil moisture storage	in	0.10	1	0.05	2	0.3	0.56-1.983	Soil properties
NSUR	Manning's n (roughness)	none	0.15	0.35	0.1	0.5	0.25-0.30	0.2-0.35	Land use, surface conditions
INTFW	Interflow/surface runoff partition parameter	none	1	3	1	10	1	0.5	Soils, topography, land use
IRC	Interflow recession parameter	none	0.5	0.7	0.3	0.85	0.3	0.3	Soils, topography, land use
LZETP	Lower zone ET parameter	none	0.2	0.7	0.1	0.9	0.2-0.6	0.1-0.7	Vegetation

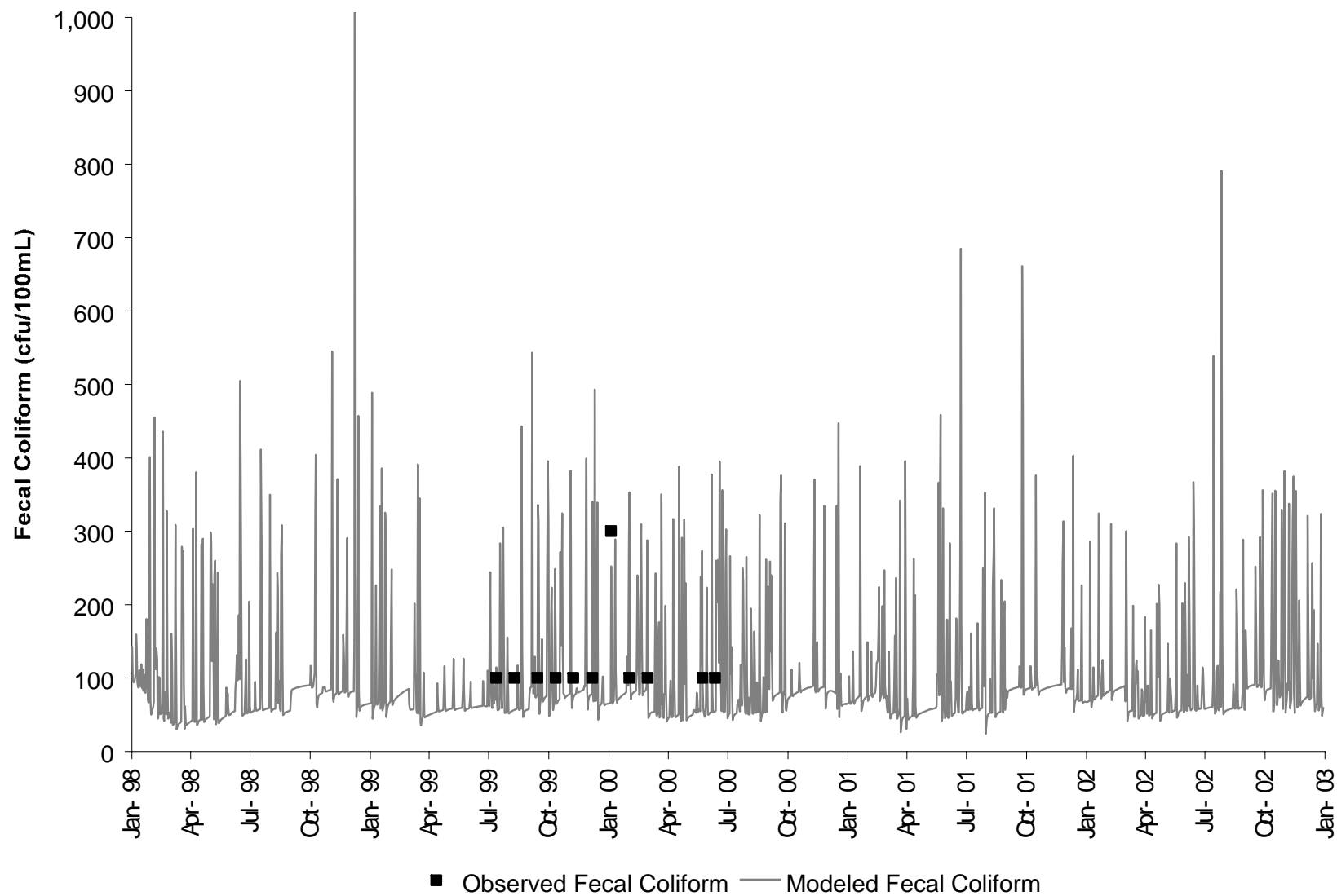
Parameter	Definition	Units	Range of Values				Start	Final	Function of...
			Typical		Possible				
			Min	Max	Min	Max			
QUAL-INPUT									
SQO	Initial storage of constituent	#/ac	0	1E20	0	1E30	4E07-3E12	4E07-3E12	Land use
ACQOP	Rate of accumulation of constituent	#/day	0	1E20	0	1E30	4E07-7E11	4E07-7E11	Land use
SQOLIM	Maximum accumulations of constituent	#/ac	0.01	1E30	0.01	1E40	2E08-3E12	4E07-21E12	Land use
WSQOP	Wash-off rate	in/hr	0.05	3.00	0.01	5.0	0.25-0.70	0.25-2.50	Land use
IOQC	Constituent concentration in interflow	#/ft <sup>3</sup>	0	1E6	0	1E10	1E03	1E03	Land use
AOQC	Constituent concentration in active groundwater	#/ft <sup>3</sup>	0	1E6	0	1E10	0E00	0E00	Land use
IMPLND									
IWAT-PARM2									
LSUR	Length of overland flow	ft	200	500	100	700	100	100	Topography
SLSUR	Slope of overland flow	none	0.01	0.15	0.001	0.3	0.01	0.01	Topography
NSUR	Manning's n (roughness)	none	0.15	0.35	0.1	0.5	0.1	0.1	Land use, surface condition
RETSC	Retention/interception storage capacity	in	0.03	0.2	0.01	0.4	0.065	0.065	Land use, surface condition
IWAT-PARM3									
PETMAX	Temp below which ET is reduced	deg. F	35	45	32	48	40	40	Climate, vegetation
PETMIN	Temp below which ET is set to zero	deg. F	30	35	30	40	35	35	Climate, vegetation
QUAL-INPUT									
SQO	Initial storage of constituent	#/ac	0	1E20	0	1E30	2E09-8E11	2E09-8E11	Land use
ACQOP	Rate of accumulation of constituent	#/day	0	1E20	0	1E30	3E08-7E10	3E08-7E10	Land use
SQOLIM	Maximum accumulations of constituent	#/ac	0.01	1E30	0.01	1E40	3E08-7E10	2E09-21E11	Land use
WSQOP	Wash-off rate	in/hr	0.05	3.00	0.01	5.0	0.1	0.1	Land use
RCHRES									
HYDR-PARM2									
KS	Weighting factor for hydraulic routing	none	0.3	0.7	0.0	0.9	0.5	0.5	Stream channel, topography
GQ-GENDECAY									
FSTDEC	First order decay rate of the constituent	1/day	0.01	10.00	0.01	30.0	1.0	0.95 - 3.00	Stream channel, environment
THFST	Temperature correction coefficient for FSTDEC	none	1	2	1	2	1.07	1.07	Water temperature



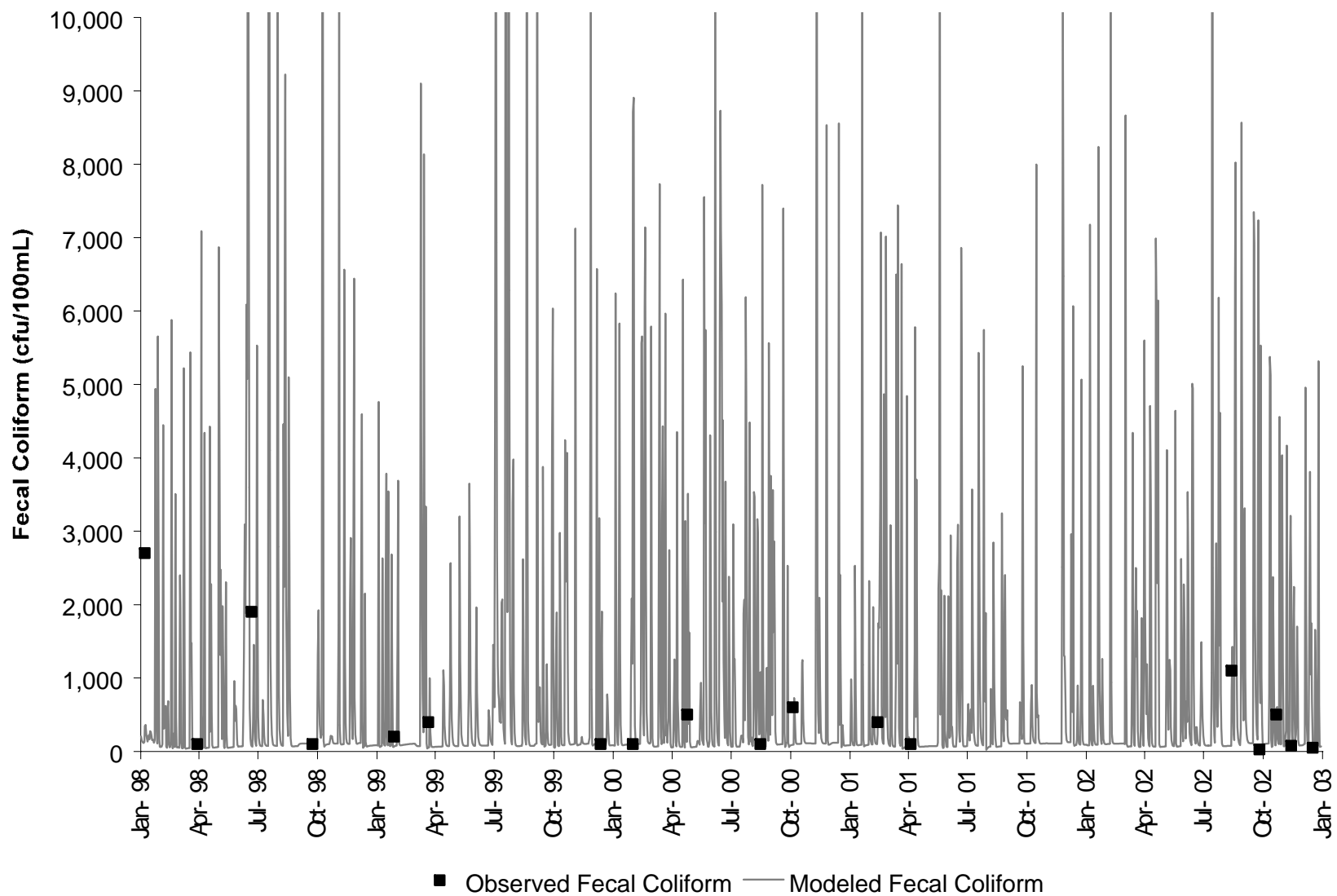
**Figure 4.10. Water quality calibration results with observed and modeled fecal coliform concentrations for subwatershed 2 in Deep Run watershed.**



**Figure 4.11. Water quality calibration results with observed and modeled fecal coliform concentrations for subwatershed 3 in Deep Run watershed.**

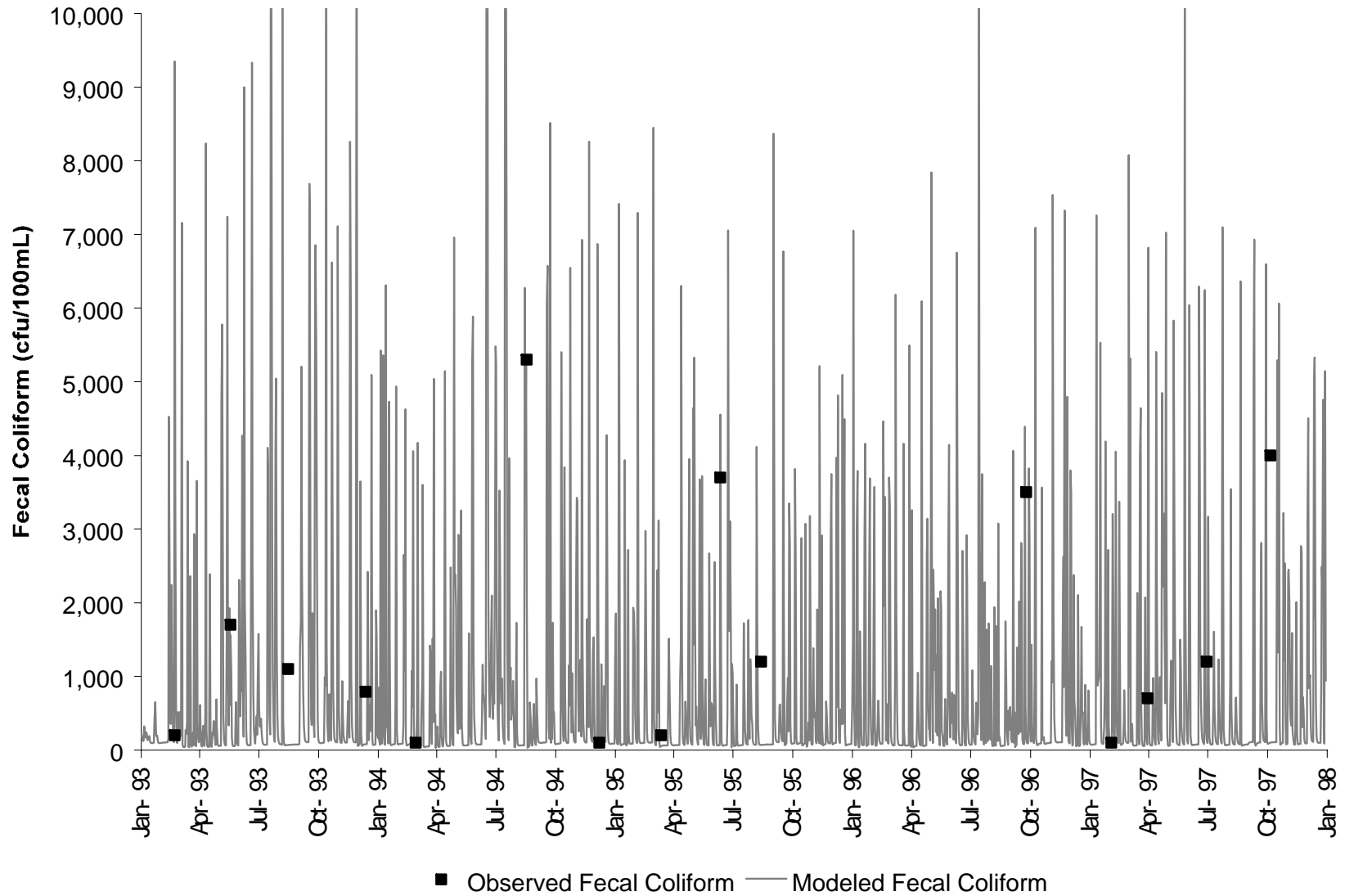


**Figure 4.12. Water quality calibration results with observed and modeled fecal coliform concentrations for subwatershed 5 in Deep Run watershed.**



**Figure 4.13. Water quality calibration results with observed and modeled fecal coliform concentrations for subwatershed 7 in Deep Run watershed.**





**Figure 4.14. Water quality validation results with observed and modeled fecal coliform concentrations for subwatershed 7 in Deep Run watershed.**

**Table 4.10. Observed and modeled geometric mean concentrations and violation rates of instantaneous standards for the calibration period in Deep Run watershed.**

<b>Parameter</b>	<b>Sub 2</b>	<b>Sub 3</b>	<b>Sub 5</b>	<b>Sub7</b>
Geometric Mean of Observed Values (cfu/100mL)	146	157	111	227
Geometric Mean of Corresponding Modeled Values (cfu/100mL)	146	154	122	251
Observed Fecal Coliform Instantaneous Standard, 1,000 cfu/100mL, Violation Rate (%)	0	10	0	17
Modeled Fecal Coliform Instantaneous Standard, 1,000 cfu/100mL, Violation Rate (%)	0	0	0	22
Observed Fecal Coliform Instantaneous Standard, 400 cfu/100mL, Violation Rate (%)	12	10	0	33
Modeled Fecal Coliform Instantaneous Standard, 400 cfu/100mL, Violation Rate (%)	12	10	0	33

**Table 4.11. Observed and modeled geometric mean concentrations and violation rates of instantaneous standards for the validation period in Deep Run watershed.**

<b>Parameter</b>	<b>Sub7</b>
Geometric Mean of Observed Values (cfu/100mL)	760
Geometric Mean of Corresponding Modeled Values (cfu/100mL)	278
Observed Fecal Coliform Instantaneous Standard, 1,000 cfu/100mL, Violation Rate (%)	53
Modeled Fecal Coliform Instantaneous Standard, 1,000 cfu/100mL, Violation Rate (%)	33
Observed Fecal Coliform Instantaneous Standard, 400 cfu/100mL, Violation Rate (%)	67
Modeled Fecal Coliform Instantaneous Standard, 400 cfu/100mL, Violation Rate (%)	33

## Chapter 5. Load Allocations

### 5.1 Background

The objective of a TMDL is to allocate allowable loads among different pollutant sources so that the appropriate control actions can be taken to achieve water quality standards (USEPA, 1991). The goal for the Deep Run TMDL was to determine what reductions in bacteria loadings from point and nonpoint sources are required to meet state water quality standards. The state water quality standards for *E. coli* used in the development of the TMDL were 126 cfu/100mL (calendar-month geometric mean) and 235 cfu/100mL (single sample maximum). The TMDL considers all sources contributing *E. coli* to Deep Run. The sources can be separated into nonpoint and point (or direct) sources. The incorporation of the different sources into the TMDL is defined in the following equation:

$$\text{TMDL} = \text{WLA} + \text{LA} + \text{MOS} \quad [5.1]$$

where:      WLA = wasteload allocation (point source contributions);  
              LA = load allocation (nonpoint source contributions); and  
              MOS = margin of safety.

While developing allocation scenarios to implement the bacteria TMDL, an implicit MOS was used by formulating conservative estimates of all factors that would affect the bacteria loadings in the watershed (e.g., animal numbers, production rates, and contributions to streams). These factors were estimated in such a way as to represent the worst-case scenario; i.e., these factors would describe the highest in-stream bacteria conditions that could exist in the watershed. Creating a TMDL with these conservative estimates ensures that the worst-case scenario has been considered and that no water quality standard violations will occur if the TMDL plan is followed.

Bacteria loadings were updated to reflect 2003 conditions for the existing conditions and allocation runs. The simulation period selected for the load allocation study was January 1993 to December 1997, which is the period that resulted in the watershed being placed on the 1998 Section 303(d) Impaired Waters List. This period incorporates average rainfall, low rainfall, and high rainfall years allowing the representation of both low and high flow conditions.

The calendar-month geometric mean values used in this report are geometric means of the daily concentrations. Because HSPF was operated with a one-hour time step in this study, 24 hourly concentrations were generated each day. To estimate the calendar-month geometric mean from the hourly HSPF output, the arithmetic mean of the hourly values was computed on a daily basis, and then the geometric mean was calculated from these average daily values.

The guidance for developing an *E. coli* TMDL put forth by the VADEQ is to develop input for the model using fecal coliform loadings as the bacteria source in the watershed. Then, the model output of average fecal coliform concentrations is converted to daily average *E. coli* concentrations through the use of the following translator equation derived by the VADEQ:

$$\log_2(\text{EC}) = -0.0172 + 0.91905 \cdot \log_2(\text{FC}) \quad [5.2]$$

where: EC = *E. coli* concentration (cfu/100mL); and  
FC = fecal coliform concentration (cfu/100mL)

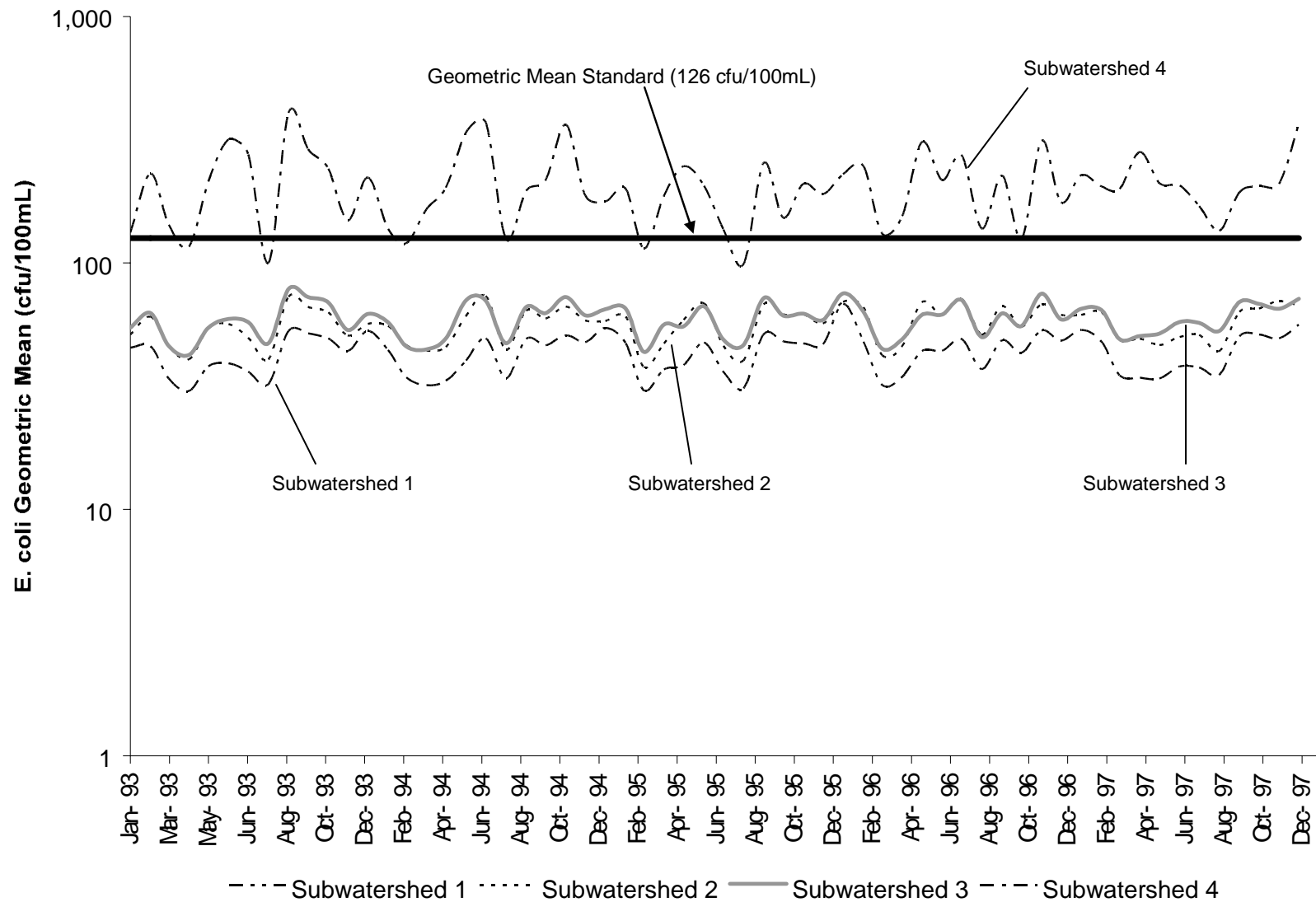
Daily *E. coli* loads were obtained by using the *E. coli* concentrations calculated from the translator equation and multiplying them by the average daily flow. Average annual loads were obtained by summing the daily loads and dividing by the number of years in the allocation period.

## 5.2 Existing Conditions

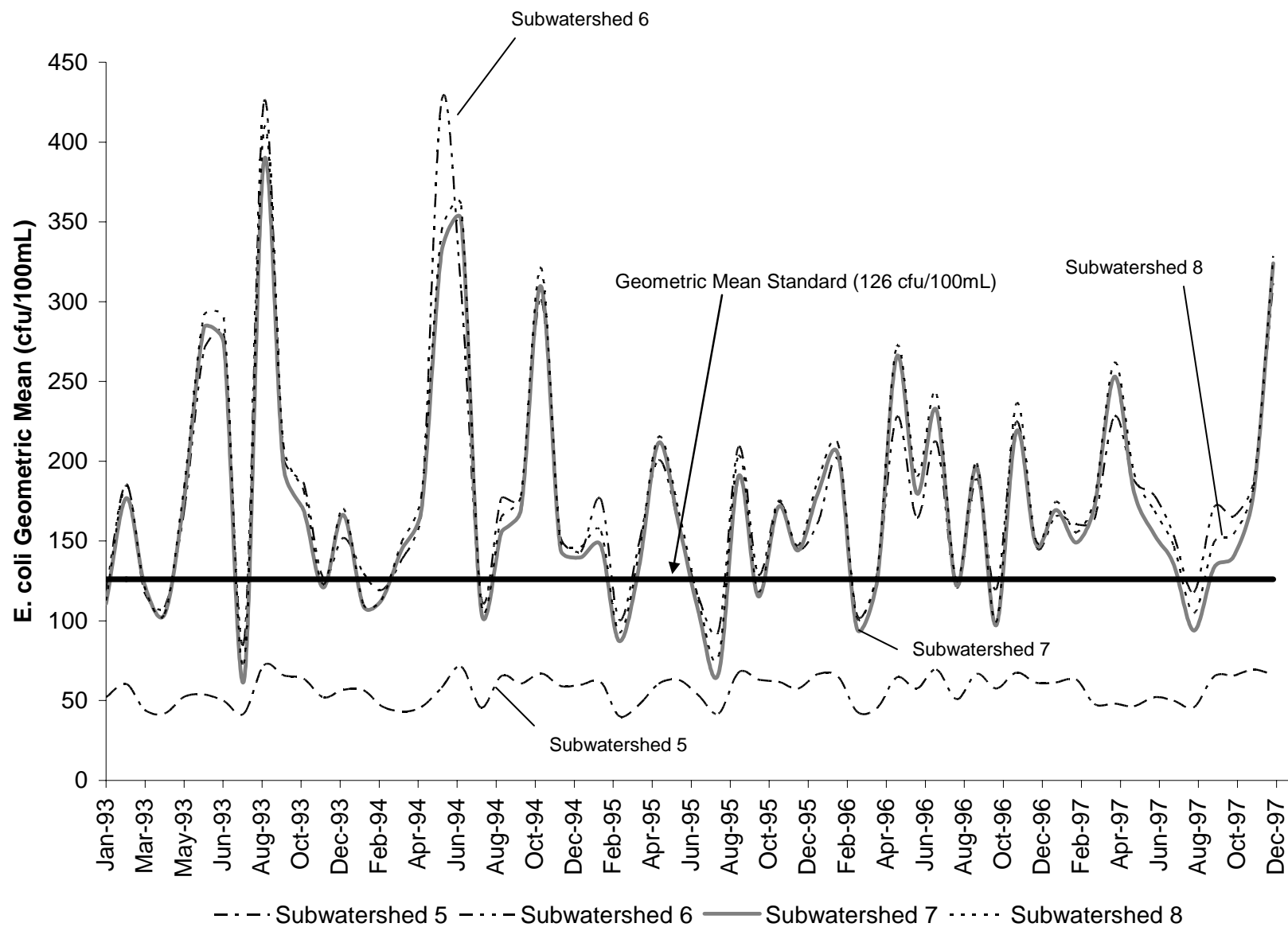
Bacteria loadings for 2003 conditions were inserted into the model and simulated for the period January 1993 to December 1997. Model output was translated to average daily *E. coli* concentrations and the monthly geometric mean was calculated. Figures 5.1 and 5.2 show the monthly geometric mean for each subwatershed in relation to the 126 cfu/100mL standard. Average daily *E. coli* concentrations at the impairment outlet (i.e., subwatershed 8) were compared to the instantaneous standard of 235 cfu/100 mL (Figure 5.3). Appendix C contains tables with monthly land-based and direct bacteria loadings for existing conditions.

## 5.3 Impact Analysis

Analyses were conducted to assess the impact of unknown variability in source allocations on changes in direct and land-based loads. Model output from existing conditions was set as the comparative base to adjustments in direct and land-based loads of +100%, +10%, -10%, and -100% of the base value. Model simulations were made for the period January 1993 to December 1997, corresponding with the period used in the allocation scenarios. Percent difference in monthly geometric mean *E. coli* concentration for each direct and land-based load change to base value was calculated and plotted in Figures 5.4 and 5.5, respectively. Figures 5.6 and 5.7, respectively, show the percent difference in the maximum daily average *E. coli* concentration per month for each direct and land-based load change to base value. Analysis results were used to assess the impact of future growth on the rate of water quality standards exceedance (Page 5-13). It is apparent by examining Figures 5.4 and 5.5 that increasing directly deposited loads impact the in-stream geometric mean *E. coli* concentrations more significantly than increasing land-based loads. Conversely, Figures 5.6 and 5.7 indicate that the maximum daily average *E. coli* concentrations are affected greatly by increasing land-based loads and very little by increasing directly deposited loads.



**Figure 5.1. Monthly *E. coli* geometric mean concentrations for existing conditions in subwatersheds 1-4 in Deep Run watershed.**



**Figure 5.2. Monthly *E. coli* geometric mean concentrations for existing conditions in subwatersheds 5-8 in Deep Run watershed.**

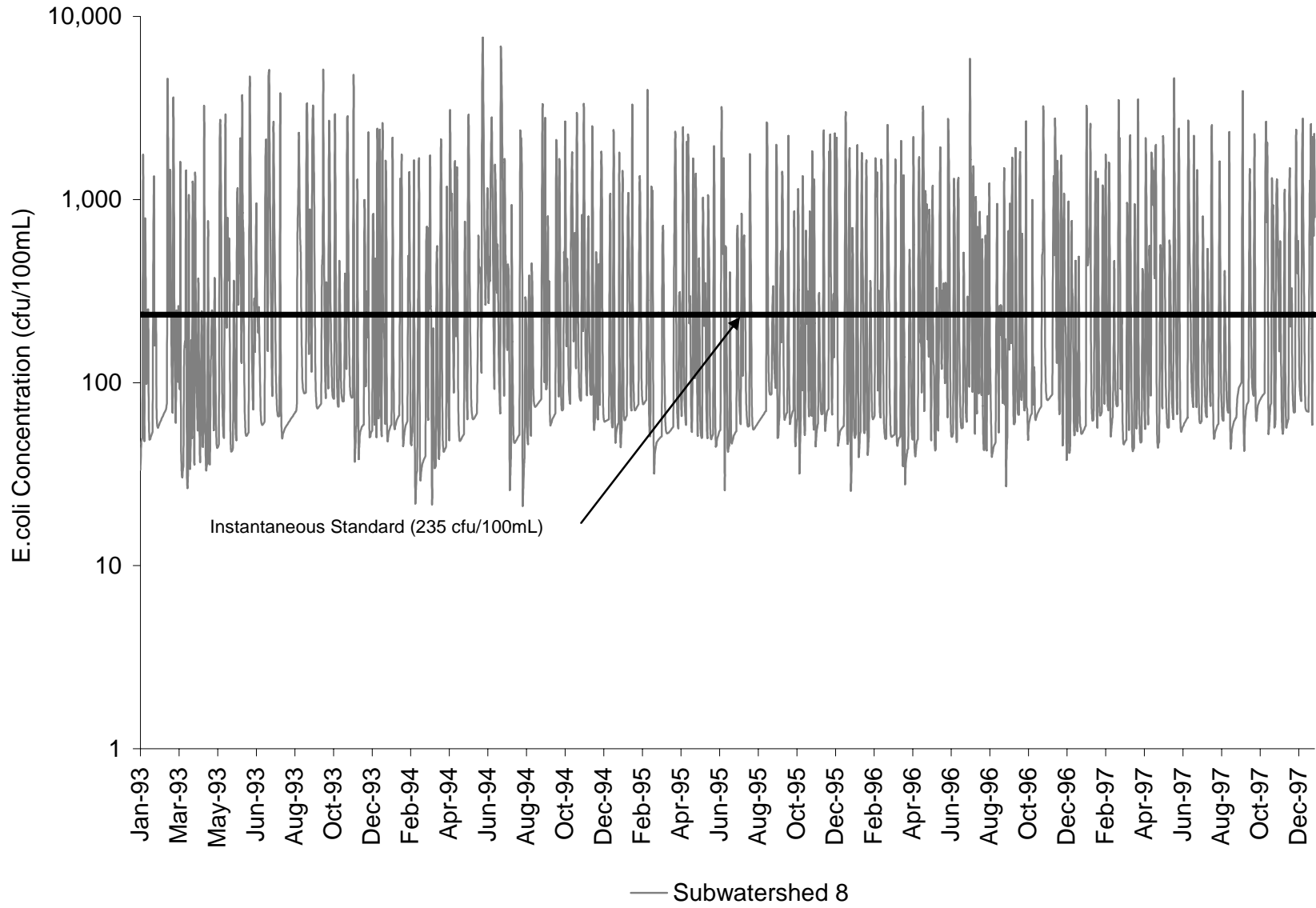
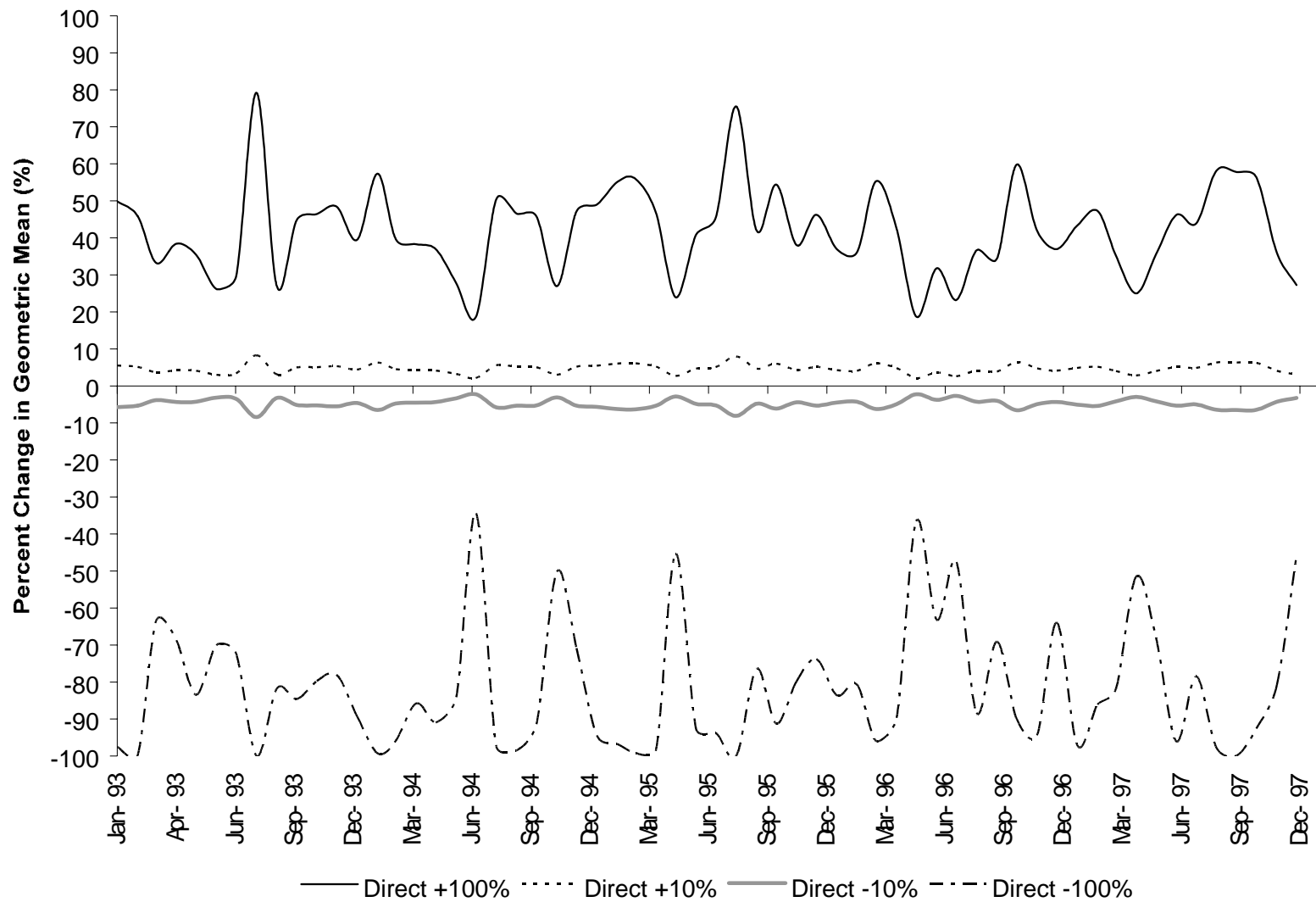
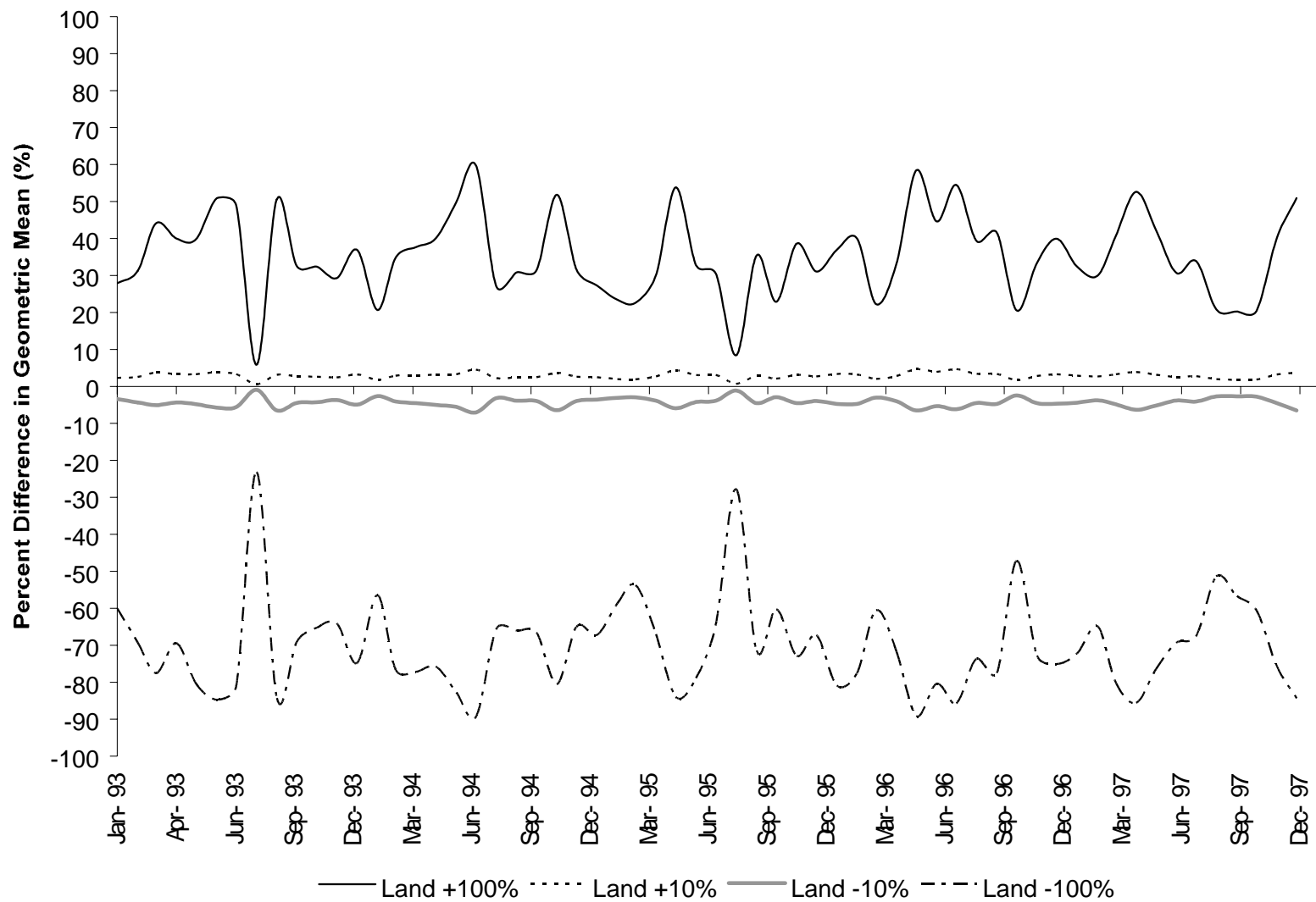


Figure 5.3. Daily average *E. coli* concentrations for subwatershed 8 in Deep Run watershed.

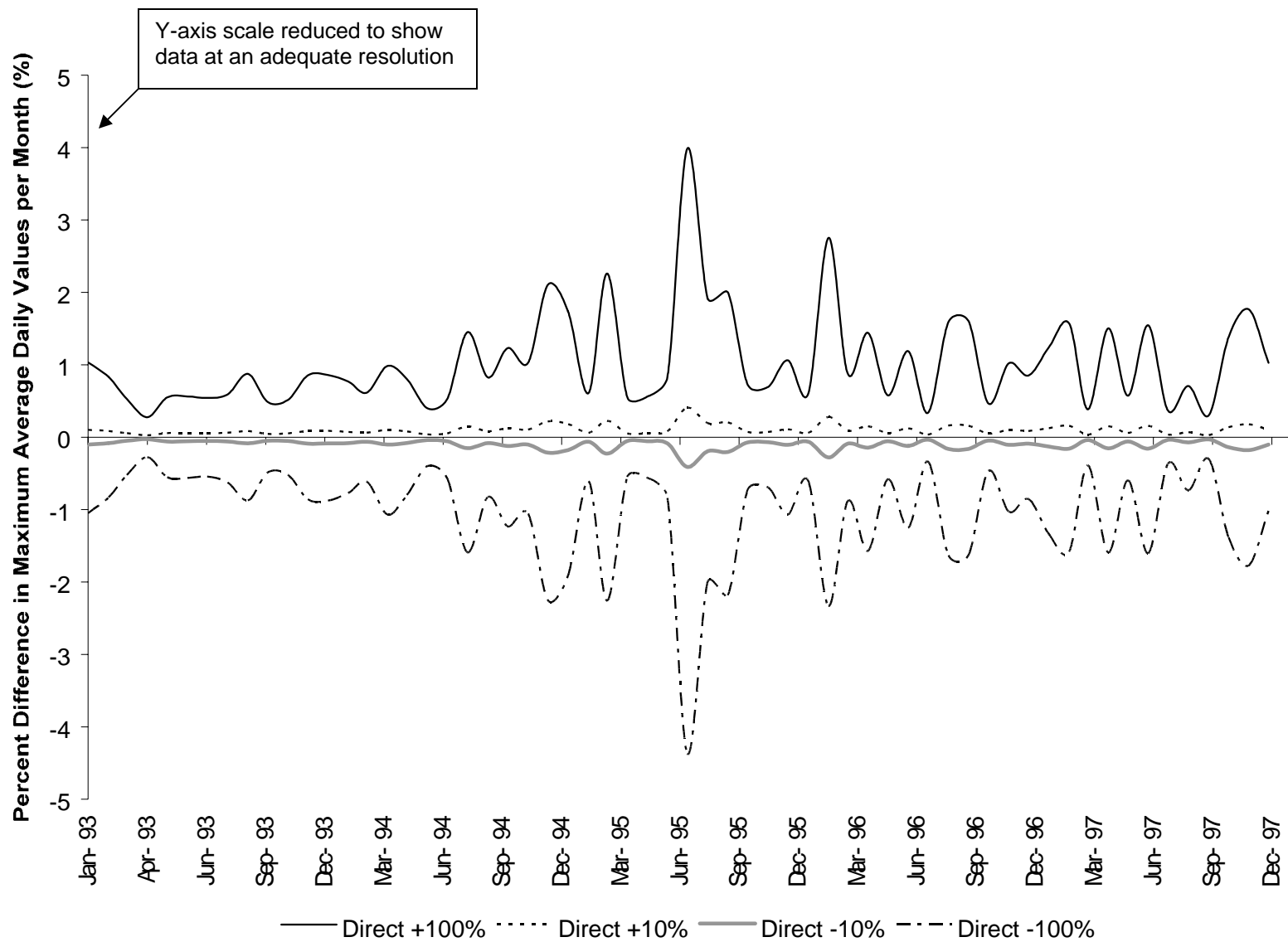


**Figure 5.4. Results of impact analysis on monthly geometric mean *E. coli* concentration at outlet (subwatershed 8) of Deep Run watershed, as affected by direct load changes.**

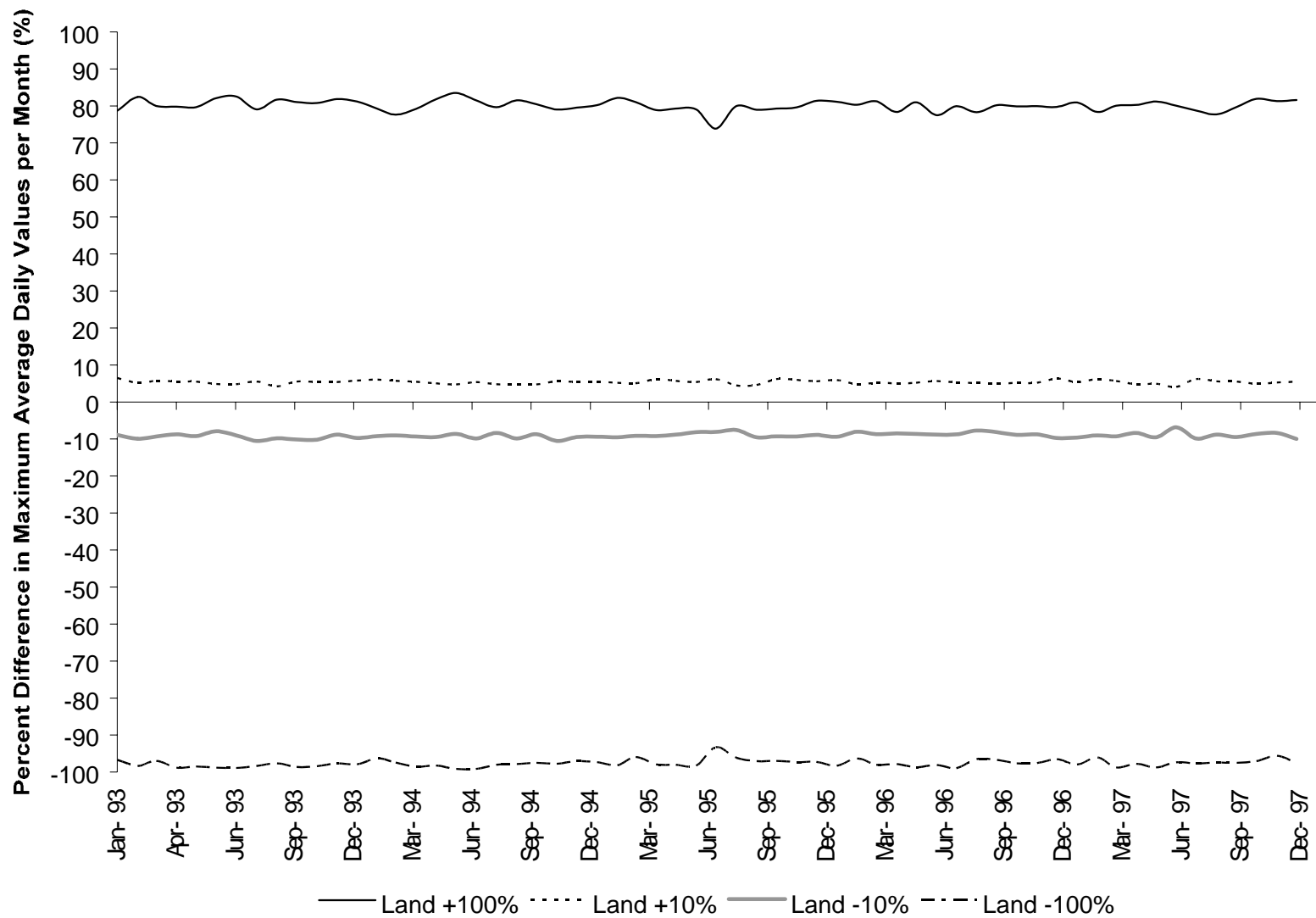




**Figure 5.5. Results of impact analysis on monthly geometric mean *E. coli* concentration at outlet (subwatershed 8) of Deep Run watershed, as affected by land-based load changes.**



**Figure 5.6. Results of impact analysis on maximum daily average *E. coli* concentration per month at outlet (subwatershed 8) of Deep Run watershed, as affected by direct load changes.**



**Figure 5.7. Results of impact analysis on maximum daily average *E. coli* concentration per month at outlet (subwatershed 8) of Deep Run watershed, as affected by land-based load changes.**

## 5.4 TMDL Allocation Scenarios

Direct and land-based loads representing existing conditions were reduced in a variety of allocation scenarios until the *E. coli* TMDL goals of a calendar-month geometric mean of 126 cfu/100mL and the instantaneous limit of 235 cfu/100mL were met. The representative modeling period selected for allocation scenarios was January 1993 to December 1997. This period incorporates average rainfall, low rainfall, and high rainfall years allowing the representation of both low and high flow conditions.

Currently, there are no point source discharges with VPDES permits or municipalities with MS4 permits within the Deep Run watershed. The resulting wasteload allocation equals zero cfu/100mL.

Scenarios to address the load allocations to non-point sources were divided between direct and land-based loadings affected by both high and low streamflow conditions. Bacterial source tracking results from samples taken during 2002-2003 confirmed the presence of human, pet, livestock, and wildlife contamination. As a result, scenarios were formulated to address reductions from all sources and delivery mechanisms. In general, direct loads modeled as consistent loadings independent of the flow regime heavily influenced low flow concentrations, whereas land-applied loads reached the stream through runoff producing events during high flow conditions. Representative allocation reduction scenarios and results are summarized in Table 5.1.

**Table 5.1. TMDL allocation scenarios for Deep Run watershed.**

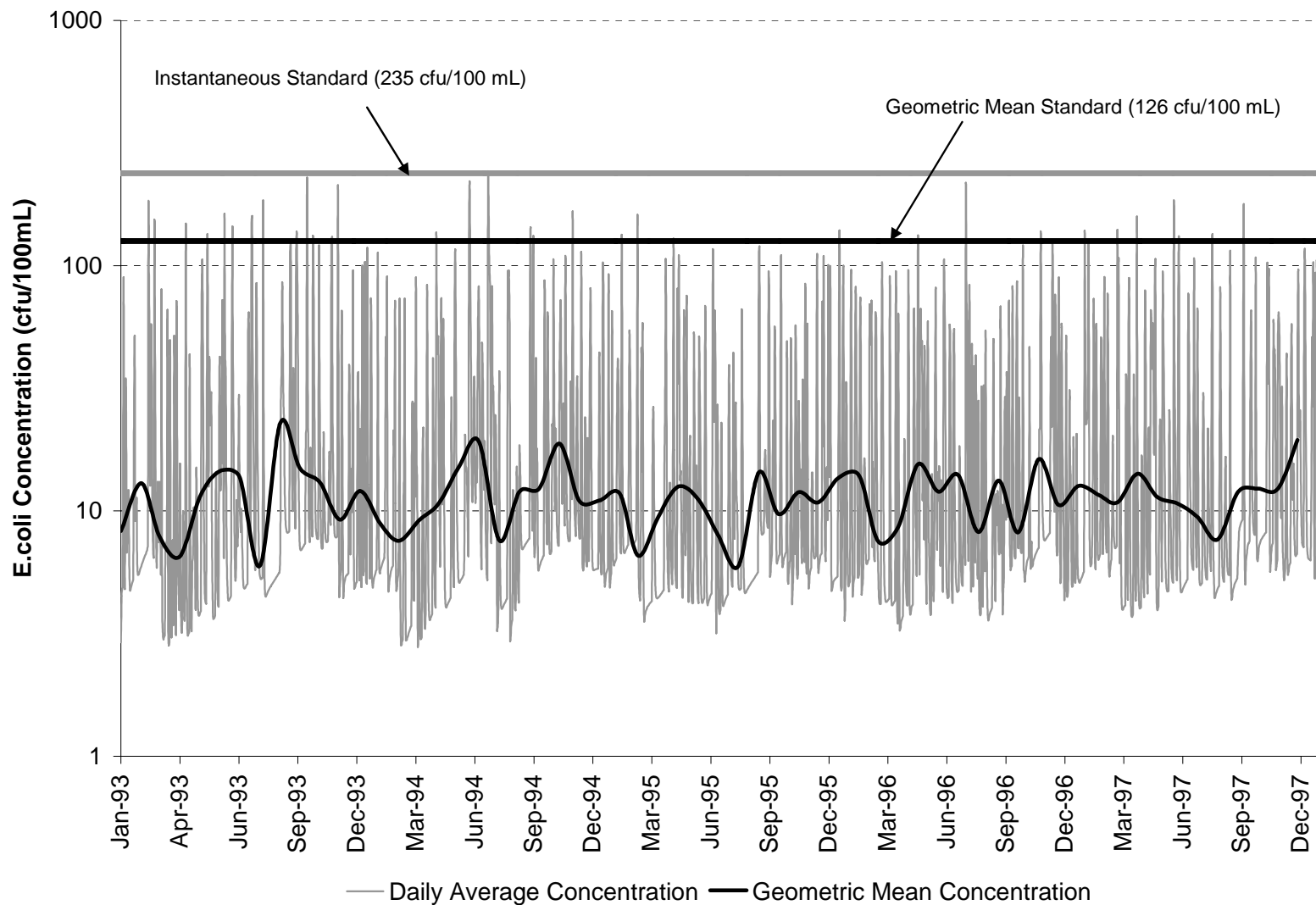
Scenario Number	Percent Reduction in Fecal Coliform Loading from Existing Conditions								% Violations of <i>E. coli</i> Standard <sup>a</sup>	
	Straight Pipes	Urban & Residential	Livestock DD	Cropland	Pasture	Loafing Lot	Wildlife DD	Forest	Geometric Mean	Instantaneous
Existing Conditions	0	0	0	0	0	N/A	0	0	75.0 (45)	34.8 (635)
1	100	50	100	50	50	N/A	0	0	28.3 (17)	25.0 (457)
2	100	99	99	99	99	N/A	0	0	0.0 (0)	0.0 (0)
3	100	0	100	0	0	N/A	100	0	6.7 (4)	32.1 (586)
4	100	95	100	95	95	N/A	75	75	0.0 (0)	1.0 (19)
5	100	98	100	98	98	N/A	100	0	0.0 (0)	0.1 (2)
6	100	98	100	98	98	N/A	90	20	0.0 (0)	0.0 (0)
7	100	98	99	99	99	N/A	0	0	0.0 (0)	0.1 (1)
8	100	99	99	99	98	N/A	0	0	0.0 (0)	0.2 (3)
<b>9</b>	<b>100</b>	<b>99</b>	<b>99</b>	<b>88</b>	<b>99</b>	<b>N/A</b>	<b>0</b>	<b>0</b>	<b>0.0 (0)</b>	<b>0.0 (0)</b>

N/A = not applicable, there is no current loading applied to loafing lot.

<sup>a</sup> Number of violations during 5-year allocation period in parentheses.

The first entry in Table 5.1 represents existing conditions in the watershed producing violations of both the geometric mean (75%) and the instantaneous standard (35%). A 100% reduction in straight pipes was used for all scenarios, since straight pipes are illegal. Reduction of loads from anthropogenic sources was investigated in Scenarios 1 and 2. Direct loadings from livestock were decreased by 100%, anthropogenic land-based loads were reduced by 50%, and direct and land-based wildlife loads were reduced by 0% for Scenario 1. Violations in the geometric mean and instantaneous standards were reduced to 28% and 25%, respectively,

a 63% and 28% reduction from existing conditions. Scenario 2 evaluated the removal of virtually all anthropogenic influence by reducing anthropogenic direct and land-based loads by 99% and reducing wildlife direct and land-based loads by 0%. Violation of both standards equaled 0%. From the BST results, wildlife was a significant source of bacteria in the watershed (Table 2.1 and Appendix B). As a result, reductions in wildlife loads were incorporated in allocation Scenarios 3 - 6. Scenario 3 evaluated the impact of direct stream loads by eliminating 100% of direct loads from straight pipes, livestock, and wildlife. Significant reduction in the geometric mean violations was achieved, however violations of the geometric mean remained (7%) along with violations in the instantaneous standard (32%). These results indicated that significant reductions in land-based contributions would be required. For Scenario 4, reductions from straight pipes and livestock direct deposition were set at 100%, reductions in nonpoint loadings to anthropogenic land uses were set at 95%, along with a 75% reduction in direct and land-based wildlife loadings producing 0% violations of the geometric mean standard and 1% violation rate of the instantaneous standard. Scenario 5 investigated the reduction of wildlife direct deposition by 100%, no reduction of loadings on forest, and increasing the reduction of nonpoint loadings on residential, cropland and pasture land uses to 98%. Geometric mean standard and instantaneous standard violation rates were 0% and 0.1%, respectively for Scenario 5. Scenario 6 met the 0% violation criteria for both standards with a 100% reduction in straight pipes and livestock direct deposition, 98% reduction in anthropogenic land-based loads, 90% reduction in wildlife direct deposition, and 20% reduction of nonpoint loadings on forest. The Scenario 6 reductions to anthropogenic sources were not significantly different from the Scenario 2 anthropogenic source reductions (i.e., 98% vs. 99%) to warrant the substantial wildlife reductions required. Reductions in the remaining scenarios (i.e., Scenarios 7 - 9) were made on individual land-based and direct loads in order to improve previous uniform reductions implemented (e.g., 99% reduction in Scenario 2). Load reductions for Scenario 2 were set as the base for Scenarios 7-9. Loads on urban/residential land uses were decreased by 98% for Scenario 7, loads on pasture were reduced by 98% for Scenario 8, and loads on cropland land use were decreased by 98% for Scenario 9. Each individual land use reduction in Scenarios 7 and 8 resulted in a 0% geometric mean violation rate and a 0.1% and 0.2% instantaneous standard violation rate, respectively. The final reduction improvement was analyzed in Scenario 9, whereby straight pipes were reduced by 100%, livestock direct deposition was reduced by 99%, nonpoint loadings to urban/residential and pasture land uses were reduced by 99%, nonpoint loadings to cropland land use were reduced by 88%, wildlife direct deposition was reduced by 0%, and nonpoint loadings on forest land use were reduced by 0%. This scenario met the 0% violation criteria of both standards and was selected as the final TMDL allocation. Concentrations for the calendar-month and daily average *E. coli* values are shown in Figure 5.8 for the final TMDL allocation (Scenario 9), along with the geometric mean and instantaneous standards. Table 5.2 lists fecal coliform loads that result in in-stream *E. coli* concentrations that meet the applicable *E. coli* water quality standards after application of the VADEQ fecal coliform to *E. coli* translator to the HSPF predicted mean daily fecal coliform concentrations. The final *E. coli* TMDL loads for the Deep Run impairment are listed in Table 5.3.



**Figure 5.8. Geometric mean standard, instantaneous single sample standard, as well as average daily and geometric mean *E. coli* concentrations from successful TMDL allocation (Allocation Scenario 9 from Table 5.1) in Deep Run watershed.**

**Table 5.2. Annual nonpoint source fecal coliform loads for existing conditions and final allocation along with corresponding reductions in Deep Run watershed.**

Source	Existing Condition Load (cfu/yr)	TMDL Allocation Load (cfu/yr)	Scenario Reduction (%)
<b>Direct</b>			
Straight Pipes	2.27E+13	0.00E+00	100
Livestock	1.92E+12	1.92E+10	99
Wildlife	7.76E+13	7.76E+13	0
<i>Total</i>	<i>1.02E+14</i>	<i>7.76E+13</i>	
<b>Land-based</b>			
Urban/Residential	6.88E+14	6.88E+12	99
Cropland	8.88E+13	1.06E+13	88
Pasture	5.08E+15	5.08E+13	99
Loafing Lot	N/A	N/A	N/A
Forest	1.95E+14	1.95E+14	0
<i>Total</i>	<i>6.05E+15</i>	<i>2.63E+14</i>	

N/A = not applicable, there is no current loading applied to loafing lot.

**Table 5.3. Average annual *E. coli* bacteria loads (cfu/yr) modeled after TMDL allocation in Deep Run watershed.**

Pollutant	WLA (cfu/yr)	LA (cfu/yr)	MOS	TMDL (cfu/yr)
Fecal Coliform	0.0	3.19E+13	N/A	3.19E+13

N/A – not applicable because MOS was implicit.

Increases in loads over the next five years must be considered to ensure the stated allocation will meet the water quality standards. It is our understanding that no major zoning changes are planned by either county that would result in accelerated development of the watershed. For purposes of this study, it was assumed that residential development in the Deep Run watershed will continue at the current rate, which is 2.2% per year, or 11.0% over five years. New housing development is expected to produce no direct deposition, and a minimal land-based load increase based on the 3% failure rate associated with new septic systems and the number of pets added by this development. Data from the VASS indicate that beef cattle populations are declining at 2.4% per year (-12% over five years), and there is no evidence that any new dairy operations are planned. Wildlife populations are expected to remain constant over the next five years. Based on these observations, it is anticipated that the increase in directly deposited and land-based loads in the Deep Run watershed will be negligible over the next five years. The effects of changes in loads on the in-stream bacteria concentration is examined in the impact analysis in Section 5.3. These changes are adequately accounted for in the implicit MOS. This implies that the final TMDL allocation is valid for the next five years, accounting for the anticipated growth during that time period.

The selected *E. coli* TMDL allocation that meets both the calendar-month geometric mean and single sample water quality goals requiring a 100% reduction in straight pipes; 99% reduction in livestock direct deposition; 99% reduction in nonpoint source loadings to urban/residential and pasture land uses; 88% reduction in nonpoint source loadings to cropland; 0% reduction in wildlife direct deposition; and 0% reduction in nonpoint source loadings to forest land addresses the following issues:

- The TMDL was developed to meet the calendar-month geometric mean and instantaneous water quality standards.
- Because *E. coli* loading data were not available to quantify point or nonpoint source bacterial loads, available fecal coliform loading data were used as input to HSPF. HSPF was used to simulate in-stream fecal coliform concentrations. The VADEQ fecal coliform to *E. coli* concentration translator was then used to convert the simulated fecal coliform concentrations to *E. coli* concentrations on which the bacteria TMDL is based.
- The TMDL was developed taking into account all fecal bacteria sources (anthropogenic and natural) from both point and nonpoint sources.
- An implicit MOS was incorporated by utilizing professional judgment and conservative estimates of model parameters.
- Both high- and low-flow stream conditions were considered while developing the TMDL.
- Both the flow regime and bacteria loading to Deep Run are seasonal. The TMDL accounts for these seasonal effects.



## **Chapter 6. TMDL Implementation and Reasonable Assurance**

### **6.1 TMDL Implementation Process**

The goal of the TMDL program is to establish a three-step path that will lead to attainment of water quality standards. The first step in this process is to develop an implementable TMDL that will result in meeting water quality standards. This report represents the culmination of that effort for the bacteria impairment in the Deep Run watershed. The second step is to develop a TMDL implementation plan, and the final step is to implement the TMDL along with monitoring stream water quality to determine if water quality standards are being attained. Watershed stakeholders will have opportunities to provide input and to participate in development of the TMDL implementation plan, with support and assistance from regional and local offices of VADEQ, VADCR, VDH, and other participating agencies.

Once a TMDL has been approved by USEPA, measures must be taken to reduce pollution levels in the stream. These measures, which can include the use of better treatment technology and the installation of best management practices (BMPs), are implemented in an iterative process that is described along with specific BMPs in the implementation plan. The process for developing an implementation plan has been described in the recent “TMDL Implementation Plan Guidance Manual,” published in July 2003 and available upon request from the VADEQ and VADCR TMDL project staff or at <http://www.deq.state.va.us/tmdl/implans/ipguide.pdf>. With successful completion of implementation plans, Virginia will be well on the way to restoring impaired waters and enhancing the value of this important resource. Additionally, development of an approved implementation plan will improve a locality's chances for obtaining financial and technical assistance during implementation.

### **6.2 Staged Implementation**

In general, the Commonwealth intends for the required reductions to be implemented in an iterative process addressing those sources with the largest impact on water quality. For example, the most promising management practice in agricultural areas of the watershed is livestock exclusion from streams. This has been shown to be very effective in lowering bacteria concentrations in streams, both from the livestock deposits themselves and additional buffering in the riparian zone. Additionally, reducing the human bacteria loading from straight pipes and failing septic systems should be a primary focus due to the health implications. This component could be implemented through education on septic tank pump-outs as well as a septic system repair/replacement program and the use of alternative waste treatment systems.

The iterative implementation of BMPs in the watershed has several benefits:

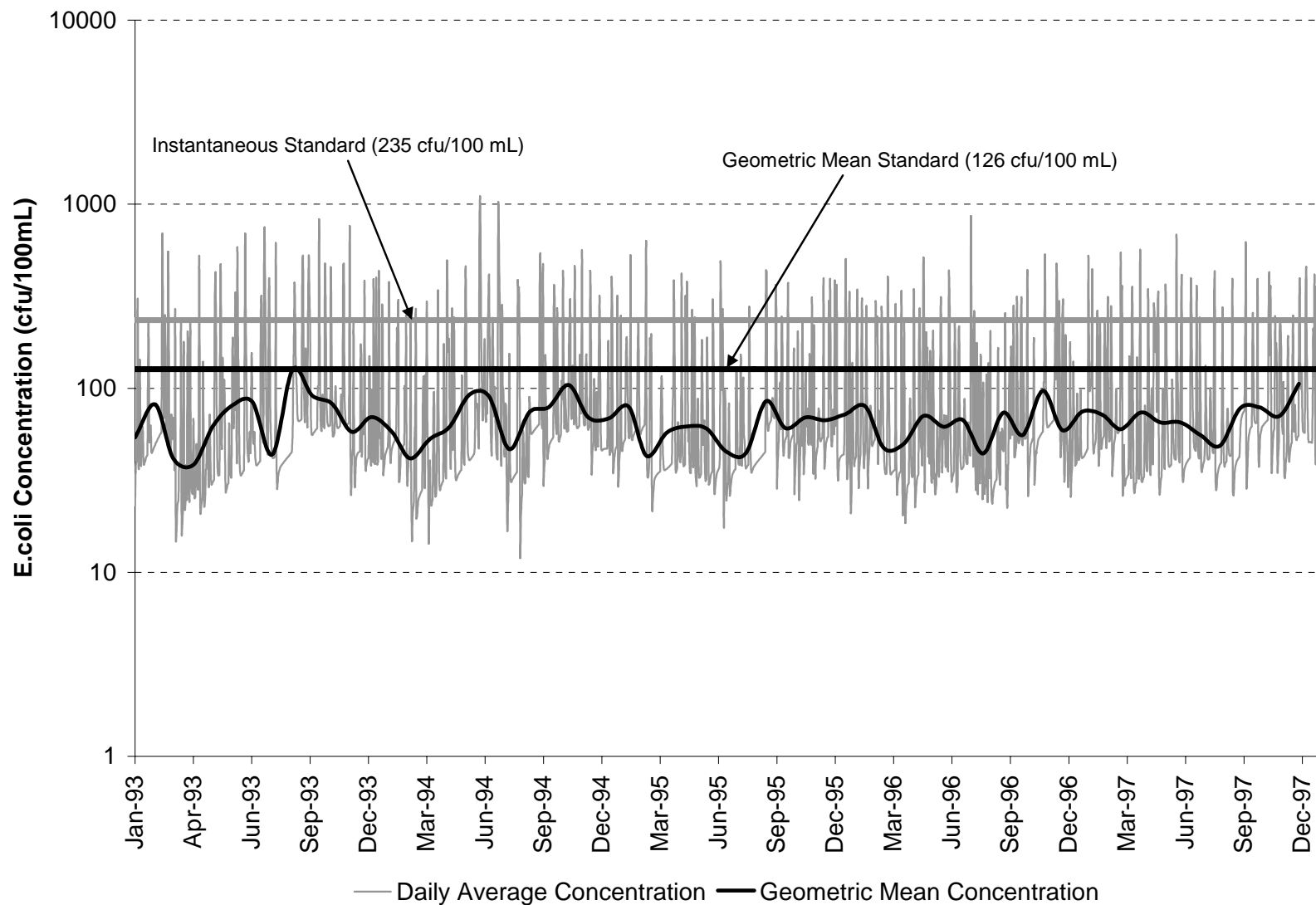
1. It enables tracking of water quality improvements following BMP implementation through follow-up stream monitoring;
2. It provides a measure of quality control, given the uncertainties inherent in computer simulation modeling;

3. It provides a mechanism for developing public support; through periodic updates on BMP implementation and water quality improvements;
4. It helps ensure that the most cost effective practices are implemented first; and
5. It allows for the evaluation of the adequacy of the TMDL in achieving water quality standards.

Watershed stakeholders will have the opportunity to participate in the development of the TMDL implementation plan. While specific goals for BMP implementation will be established as part of the implementation plan development, the following Stage 1 scenarios are targeted at controllable, anthropogenic bacteria sources and can serve as starting points for targeting BMP implementation activities.

### **6.3 Stage 1 Scenarios**

The goal of the Stage 1 implementation scenarios was to determine the bacteria loading reductions from controllable sources required to reduce violations of the single sample 235 cfu/100mL water quality standard to less than 10 percent with no reduction from wildlife sources. For the implementation scenarios, HSPF was run with a one-hour time step for the period January 1993 to December 1997, as with the TMDL allocation scenarios. The implicit MOS used in allocation scenarios was utilized in determining the Stage 1 implementation scenarios. Several scenarios were run until the Stage 1 goal was met. The Stage 1 allocation requires a 100% reduction in straight pipes, 99% reduction in livestock direct deposition, and 88% reduction in nonpoint source loadings to urban/residential, cropland, and pasture land uses. This scenario resulted in a 0% geometric mean standard violation rate and a 9.8% instantaneous standard violation rate. Fecal coliform loadings for the existing allocation and Stage 1 allocation scenario for nonpoint sources by land use and direct nonpoint sources are presented in Table 6.1. *E. coli* concentrations resulting from application of the fecal coliform to *E. coli* translator equation to the fecal coliform loads from the final scenario are presented graphically in Figure 6.1.



**Figure 6.1. Geometric mean standard, instantaneous single sample standard, as well as average daily and geometric mean *E. coli* concentrations for the Stage 1 TMDL implementation scenario in Deep Run watershed.**

**Table 6.1. Annual nonpoint source fecal coliform loads for existing conditions and Stage 1 TMDL implementation scenario along with corresponding reductions in Deep Run watershed.**

Source	Existing Condition Load (cfu/yr)	Stage 1 Allocation Load (cfu/yr)	Scenario Reduction (%)
<b>Direct</b>			
Straight Pipes	2.27E+13	0.00E+00	100
Livestock	1.92E+12	1.92E+10	99
Wildlife	7.76E+13	7.76E+13	0
<b>Land-based</b>			
Urban/Residential	6.88E+14	8.26E+13	88
Cropland	8.88E+13	1.07E+13	88
Pasture	5.08E+15	6.10E+14	88
Loafing Lot	N/A	N/A	N/A
Forest	1.95E+14	1.95E+14	0

N/A = not applicable, there is no current loading applies to loafing lot.

## 6.4 Link to Ongoing Restoration Efforts

Implementation of this TMDL will contribute to on-going water quality improvement efforts aimed at restoring water quality in the Chesapeake Bay. Several BMPs known to be effective in controlling bacteria have also been identified for implementation as part of the 2001 Interim Nutrient Cap Strategy for the Rappahannock River Basin. For example, management of on-site waste management systems, management of livestock and manure, and pet waste management are among the components of the strategy described under nonpoint source implementation mechanisms (2001 Draft Interim Nutrient Cap Strategy for the Rappahannock River Basin). A new draft tributary strategy is currently available for the Rappahannock River Basin to address the nutrient and sediment reductions required to restore the health of the Chesapeake Bay. Up-to-date information can be found at the tributary strategy web site under <http://www.snr.state.va.us/Initiatives/TributaryStrategies/rappahannock.cfm>.

## 6.5 Reasonable Assurance for Implementation

### 6.5.1 Follow-up Monitoring

VADEQ will continue monitoring Deep Run at station 3-DPR001.70 in accordance with its ambient monitoring program to evaluate reductions in fecal bacteria counts and the effectiveness of TMDL implementation in attainment of water quality standards. The station on Deep Run is a trend station and will be monitored on a monthly basis. Plans for additional monitoring to assess the effectiveness of implementation actions will be developed as part of the implementation planning process.

### **6.5.2 Regulatory Framework**

While Section 303(d) of the Clean Water Act and current USEPA regulations do not require the development of TMDL implementation plans as part of the TMDL process, they do require reasonable assurance that the load and wasteload allocations can and will be implemented. Additionally, Virginia's 1997 Water Quality Monitoring, Information and Restoration Act (the "Act") directs the State Water Control Board to "develop and implement a plan to achieve fully supporting status for impaired waters" (Section 62.1-44.19.7). The Act also establishes that the implementation plan shall include the date of expected achievement of water quality objectives, measurable goals, corrective actions necessary and the associated costs, benefits and environmental impacts of addressing the impairments. USEPA outlines the minimum elements of an approvable implementation plan in its 1999 "Guidance for Water Quality-Based Decisions: The TMDL Process." The listed elements include implementation actions/management measures, timelines, legal or regulatory controls, time required to attain water quality standards, monitoring plans and milestones for attaining water quality standards.

Watershed stakeholders will have opportunities to provide input and to participate in the development of the implementation plan, which will also be supported by regional and local offices of VADEQ, VADCR, and other cooperating agencies.

VADEQ intends to incorporate TMDL implementation plans into the appropriate Water Quality Management Plan (WQMP), in accordance with the Clean Water Act's Section 303(e). In response to the recent USEPA/VADEQ/VADCR Memorandum of Understanding, VADEQ submitted a Continuous Planning Process to USEPA in which VADEQ commits to regularly updating the WQMPs. Thus, the WQMPs will be, among other things, the repository for all TMDLs and TMDL implementation plans developed within a river basin.

### **6.5.3 Funding Sources**

One potential source of funding for TMDL implementation is Section 319 of the Clean Water Act. In response to the federal Clean Water Action Plan, Virginia developed a Unified Watershed Assessment that identifies watershed priorities. Watershed restoration activities, such as TMDL implementation, within these priority watersheds are eligible for Section 319 funding. An increasing proportion of Section 319 funding in future years will be targeted towards TMDL implementation and watershed restoration. Additional funding sources for implementation may include the U.S. Department of Agriculture Conservation Reserve Enhancement and Environmental Quality Incentives Programs, the Virginia State Revolving Loan Program, and the Virginia Water Quality Improvement Fund. The TMDL Implementation Plan Guidance Manual contains additional information on funding sources, as well as government agencies that might support implementation efforts and suggestions for integrating TMDL implementation with other watershed planning efforts.

### **6.5.4 Addressing Wildlife Contributions**

In some streams for which TMDLs have been developed, water quality modeling indicates that even after removal of all bacteria sources (other than wildlife), the stream will not attain standards under all flow regimes at all times. These streams may not be able to attain

standards without some reduction in wildlife load. **Virginia and USEPA are not proposing the elimination of wildlife to allow for the attainment of water quality standards.** While managing overpopulations of wildlife remains an option to local stakeholders, the reduction of wildlife or changing a natural background condition is not the intended goal of a TMDL.

To address this issue, Virginia proposed (during its recent triennial water quality standards review) a new “secondary contact” category for protecting the recreational use in state waters. On March 25, 2003, the Virginia State Water Control Board adopted criteria for “secondary contact recreation” which means “a water-based form of recreation, the practice of which has a low probability for total body immersion or ingestion of waters (examples include but are not limited to wading, boating and fishing).” These new criteria were approved by USEPA and became effective on February 12, 2004 (<http://www.deq.state.va.us/wqs/rule.html>).

In order for the new criteria to apply to a specific stream segment, the primary contact recreational use must be removed. To remove a designated use, the state must demonstrate 1) that the use is not an existing use, 2) that downstream uses are protected, and 3) that the source of bacterial contamination is natural and uncontrollable by effluent limitations and by implementing cost-effective and reasonable best management practices for nonpoint source control (9 VAC 25-260-10). This and other information is collected through a special study called a Use Attainability Analysis (UAA). All site-specific criteria or designated use changes must be adopted as amendments to the water quality standards regulations. Watershed stakeholders and USEPA will be able to provide comment during this process. Additional information can be obtained at <http://www.deq.state.va.us/wqs/WQS03AUG.pdf>

Based on the above, USEPA and Virginia have developed a process to address the wildlife issue. First in this process is the development of a Stage 1 scenario such as those presented previously in this chapter. The pollutant reductions in the Stage 1 scenario are targeted only at the controllable, anthropogenic bacteria sources identified in the TMDL, setting aside control strategies for wildlife except for cases of overpopulation. During the implementation of the Stage 1 scenario, all controllable sources would be reduced to the maximum extent practicable using the iterative approach described in Section 6.1 above. VADEQ will re-assess water quality in the stream during and subsequent to the implementation of the Stage 1 scenario to determine if the water quality standard is attained. This effort will also evaluate if the modeling assumptions were correct. If water quality standards are not being met, a UAA may be initiated to reflect the presence of naturally high bacteria levels due to uncontrollable sources. In some cases, the effort may never have to go to the UAA phase because the water quality standard exceedances attributed to wildlife in the model may have been very small and infrequent and within the margin of error.

## **Chapter 7. Public Participation**

The development of the Deep Run TMDL would not have been possible without public participation. The first public meeting was held at the Mary Walter Elementary School in Bealeton on April 2, 2003 to discuss the need for a TMDL and the process for TMDL development. Twelve people attended. Copies of the presentation materials were available for public distribution. Public notice of the meeting was printed in the Virginia Register, as well as in the Fauquier Times-Democrat and the Fredericksburg Freelance Star. A postcard mailing announcing the meeting was sent to watershed residents, and the meeting advertised on the VADEQ and Rappahannock-Rapidan Regional Commission websites. There was a 30-day public comment period and no written comment was received.

The second public meeting was also held at the Mary Walter Elementary School on September 17, 2003 to discuss the draft watershed source assessment and to review the approach for TMDL development. Eight people attended. Public notice of the meeting was printed in the Virginia Register and included in the community calendars of the Fauquier Times-Democrat and the Fredericksburg Freelance Star. A newsletter announcing the meeting was sent to prior meeting attendees, and the meeting advertised on the VADEQ and Rappahannock-Rapidan Regional Commission websites. In addition, flyers inviting the public to attend the meeting were distributed through the John Marshall and Tri-City/County Soil and Water Conservation District offices, and posted at various locations around the watershed. There was a 30-day public comment period and no written comments were received.

The third and final public meeting was again held at the Mary Walter Elementary School on March 10, 2004 to discuss the source allocations and reductions required to meet the TMDL. Ten people attended. Copies of the draft TMDL report were available for public review and comment. Public notice of the meeting was printed in the Virginia Register and included in the community calendars of the Fauquier Citizen, Fauquier Times-Democrat and the Fredericksburg Freelance Star. A postcard mailing announcing the meeting was sent to watershed residents and a newsletter announcing the meeting was sent to area appointed and elected officials and prior meeting attendees. There was a 30-day public comment period and one written comment was received.

In addition to keeping the public apprised of progress in the development of the Deep Run TMDL, a Technical Advisory Committee (TAC) was also established to help advise the TMDL developers. TAC meetings were held two to three weeks prior to public meetings. The TAC membership included representatives from the following agencies and organizations:

- Virginia Department of Environmental Quality
- Virginia Department of Conservation and Recreation
- Virginia Department of Game and Inland Fisheries
- Culpeper County Planning
- Fauquier County Planning

- Stafford County Planning
- Culpeper SWCD
- John Marshall SWCD
- Tri-City/County SWCD
- VA Cooperative Extension
- Natural Resources Conservation Service
- Friends of the Rappahannock

The Deep Run TAC met on February 21, 2003, August 21, 2003, and February 25, 2004, to discuss the Deep Run bacteria TMDL. TAC meetings were used as a forum to review data and assumptions used in the modeling, and to provide local government agencies an opportunity to raise concerns about the implications of the TMDL for their jurisdictions. The generous assistance of the staff of these agencies is gratefully acknowledged.



# Glossary

Adopted from an USEPA-Approved TMDL prepared by the Virginia Tech BSE Department

## **Allocation**

That portion of a receiving water's loading capacity that is attributed to one of its existing or future pollution sources (nonpoint or point) or to natural background sources.

## **Allocation Scenario**

A proposed series of point and nonpoint source allocations (loadings from different sources), which are being considered to meet a water quality planning goal.

## **Background levels**

Levels representing the chemical, physical, and biological conditions that would result from natural geomorphological processes such as weathering and dissolution. A computer-run tool that contains an assessment and planning component that allows users to organize and display geographic information for selected watersheds. It also contains a modeling component to examine impacts of pollutant loadings from point and nonpoint sources and to characterize the overall condition of specific watersheds.

## **Best Management Practices (BMP)**

Methods, measures, or practices that are determined to be reasonable and cost-effective means for a land owner to meet certain, generally nonpoint source, pollution control needs. BMPs include structural and nonstructural controls and operation and maintenance procedures.

## **Bacterial Source Tracking (BST)**

A collection of scientific methods used to track sources of fecal coliform.

## **Calibration**

The process of adjusting model parameters within physically defensible ranges until the resulting predictions give a best possible good fit to observed data.

## **Die-off (of fecal coliform)**

Reduction in the fecal coliform population due to predation by other bacteria as well as by adverse environmental conditions (e.g., UV radiation, pH).

## **Direct nonpoint sources**

Sources of pollution that are defined statutorily (by law) as nonpoint sources that are represented in the model as point source loadings due to limitations of the model. Examples include: direct deposits of fecal material to streams from livestock and wildlife.

## **E-911 digital data**

Emergency response database prepared by the county that contains graphical data on road centerlines and buildings. The database contains approximate outlines of buildings, including dwellings and poultry houses.

## **Failing septic system**

Septic systems in which drain fields have failed such that effluent (wastewater) that is supposed

to percolate into the soil, now rises to the surface and ponds on the surface where it can flow over the soil surface to streams or contribute pollutants to the surface where they can be lost during storm runoff events.

### **Fecal coliform**

A type of bacteria found in the feces of various warm-blooded animals that is used as indicator of the possible presence of pathogenic (disease causing) organisms.

### **Geometric mean**

The geometric mean is simply the nth root of the product of n values. Using the geometric mean, lessens the significance of a few extreme values (extremely high or low values). In practical terms, this means that if you have just a few bad samples, their weight is lessened.

Mathematically the geometric mean,  $\bar{x}_g$ , is expressed as:  $\bar{x}_g = \sqrt[n]{x_1 \cdot x_2 \cdot x_3 \dots x_n}$  where n is the number of samples, and  $x_i$  is the value of sample i.

### **HSPF (Hydrological Simulation Program-Fortran)**

A computer-based model that calculates runoff, sediment yield, and fate and transport of various pollutants to the stream. The model was developed under the direction of the U.S. Environmental Protection Agency (EPA).

### **Hydrology**

The study of the distribution, properties, and effects of water on the earth's surface, in the soil and underlying rocks, and in the atmosphere.

### **Instantaneous criterion**

The instantaneous criterion or instantaneous water quality standard is the value of the water quality standard that should not be exceeded at any time. For example, the Virginia instantaneous water quality standard for fecal coliform is 1,000 cfu/100 mL. If this value is exceeded at any time, the water body is in violation of the state water quality standard.

### **Load allocation (LA)**

The portion of a receiving water's loading capacity that is attributed either to one of its existing or future nonpoint sources of pollution or to natural background.

### **Margin of Safety (MOS)**

A required component of the TMDL that accounts for the uncertainty about the relationship between the pollutant loads and the quality of the receiving waterbody. The MOS is normally incorporated into the conservative assumptions used to develop TMDLs (generally within the calculations or models). The MOS may also be assigned explicitly, as was done in this study, to ensure that the water quality standard is not violated.

### **Model**

Mathematical representation of hydrologic and water quality processes. Effects of Land use, slope, soil characteristics, and management practices are included.

### **Nonpoint source**

Pollution that is not released through pipes but rather originates from multiple sources over a

relatively large area. Nonpoint sources can be divided into source activities related to either land or water use including failing septic tanks, improper animal-keeping practices, forest practices, and urban and rural runoff.

**Pathogen**

Disease-causing agent, especially microorganisms such as bacteria, protozoa, and viruses.

**Point source**

Pollutant loads discharged at a specific location from pipes, outfalls, and conveyance channels from either municipal wastewater treatment plants or industrial waste treatment facilities. Point sources can also include pollutant loads contributed by tributaries to the main receiving water stream or river.

**Pollution**

Generally, the presence of matter or energy whose nature, location, or quantity produces undesired environmental effects. Under the Clean Water Act for example, the term is defined as the man-made or man-induced alteration of the physical, biological, chemical, and radiological integrity of water.

**Reach**

Segment of a stream or river.

**Runoff**

That part of rainfall or snowmelt that runs off the land into streams or other surface water. It can carry pollutants from the air and land into receiving waters.

**Septic system**

An on-site system designed to treat and dispose of domestic sewage. A typical septic system consists of a tank that receives liquid and solid wastes from a residence or business and a drainfield or subsurface absorption system consisting of a series of tile or percolation lines for disposal of the liquid effluent. Solids (sludge) that remain after decomposition by bacteria in the tank must be pumped out periodically.

**Simulation**

The use of mathematical models to approximate the observed behavior of a natural water system in response to a specific known set of input and forcing conditions. Models that have been validated, or verified, are then used to predict the response of a natural water system to changes in the input or forcing conditions.

**Straight pipe**

Delivers wastewater directly from a building, e.g., house, milking parlor, to a stream, pond, lake, or river.

**Total Maximum Daily Load (TMDL)**

The sum of the individual wasteload allocations (WLA's) for point sources, load allocations (LA's) for nonpoint sources and natural background, plus a margin of safety (MOS). TMDLs can be expressed in terms of mass per time, toxicity, or other appropriate measures that relate to a state's water quality standard.

**Urban Runoff**

Surface runoff originating from an urban drainage area including streets, parking lots, and rooftops.

**Validation (of a model)**

Process of determining how well the mathematical model's computer representation describes the actual behavior of the physical process under investigation.

**Wasteload allocation (WLA)**

The portion of a receiving water's loading capacity that is allocated to one of its existing or future point sources of pollution. WLAs constitute a type of water quality-based effluent limitation.

**Water quality standard**

Law or regulation that consists of the beneficial designated use or uses of a water body, the numeric and narrative water quality criteria that are necessary to protect the use or uses of that particular water body, and an anti-degradation statement.

**Watershed**

A drainage area or basin in which all land and water areas drain or flow toward a central collector such as a stream, river, or lake at a lower elevation.

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## **Appendix A – Historic Water Quality Data**



**Table A.1. Observed fecal coliform concentration and antecedent rainfall for VADEQ station 3DPR001.70 in Deep Run watershed.**

<b>Station</b>	<b>Date</b>	<b>Observed Fecal Coliform Concentration (cfu/100mL)</b>	<b>Total Rainfall for Sampling Day and Preceding 5 Days (in)</b>
3DPR001.70	8/29/91	45	0
3DPR001.70	2/27/92	490	2
3DPR001.70	9/14/92	400	0.9
3DPR001.70	12/1/92	100	0.2
3DPR001.70	2/22/93	200	1
3DPR001.70	5/19/93	1,700	1.4
3DPR001.70	8/16/93	1,100	0
3DPR001.70	12/13/93	790	0
3DPR001.70	2/28/94	100	2.2
3DPR001.70	8/18/94	5,300	4.4
3DPR001.70	12/8/94	100	1.4
3DPR001.70	3/13/95	200	2.2
3DPR001.70	6/12/95	3,700	2.2
3DPR001.70	8/14/95	1,200	0
3DPR001.70	9/25/96	3,500	0.3
3DPR001.70	2/3/97	100	0
3DPR001.70	3/31/97	700	0.7
3DPR001.70	6/30/97	1,200	2.9
3DPR001.70	10/6/97	4,000	0
3DPR001.70	1/8/98	2,700	0.7
3DPR001.70	3/30/98	100	0
3DPR001.70	6/22/98	1,900	0.1
3DPR001.70	9/24/98	100	0
3DPR001.70	1/28/99	200	1.81
3DPR001.70	3/22/99	400	2
3DPR001.70	12/13/99	100	1
3DPR001.70	2/1/00	100	0.9
3DPR001.70	4/25/00	500	1.6
3DPR001.70	8/16/00	100	0.11
3DPR001.70	10/5/00	600	0
3DPR001.70	2/13/01	400	0.1
3DPR001.70	4/5/01	100	0.1
3DPR001.70	8/13/02	1,100	0.1
3DPR001.70	9/25/02	25	0.32
3DPR001.70	10/22/02	500	0.52
3DPR001.70	11/14/02	75	1.87
3DPR001.70	12/17/02	50	0.86

**Table A.2. Observed fecal coliform concentration and antecedent rainfall for VADEQ station 3DPR004.93 in Deep Run watershed.**

Station	Date	Observed Fecal Coliform Concentration (cfu/100mL)	Total Rainfall for Sampling Day and Preceding 5 Days (in)
3DPR004.93	7/13/99	300	0.6
3DPR004.93	8/10/99	100	0
3DPR004.93	9/14/99	100	1.3
3DPR004.93	10/12/99	100	0.42
3DPR004.93	11/8/99	100	1.09
3DPR004.93	12/7/99	100	0.5
3DPR004.93	1/5/00	3,100	0.3
3DPR004.93	2/2/00	100	0.9
3DPR004.93	3/1/00	100	0.76
3DPR004.93	5/24/00	100	1.732

**Table A.3. Observed fecal coliform concentration and antecedent rainfall for VADEQ station 3DPR008.98 in Deep Run watershed.**

Station	Date	Observed Fecal Coliform Concentration (cfu/100mL)	Total Rainfall for Sampling Day and Preceding 5 Days (in)
3DPR008.98	7/13/99	300	0.6
3DPR008.98	10/12/99	100	0.42
3DPR008.98	11/8/99	100	1.09
3DPR008.98	12/7/99	100	0.5
3DPR008.98	1/5/00	700	0.3
3DPR008.98	3/1/00	100	0.76
3DPR008.98	5/24/00	100	1.732
3DPR008.98	6/12/00	100	0

**Table A.4. Observed fecal coliform concentration and antecedent rainfall for VADEQ station 3ALC002.74 in Deep Run watershed.**

<b>Station</b>	<b>Date</b>	<b>Observed Fecal Coliform Concentration (cfu/100mL)</b>	<b>Total Rainfall for Sampling Day and Preceding 5 Days (in)</b>
3ALC002.74	7/13/99	100	0.6
3ALC002.74	8/10/99	100	0
3ALC002.74	9/14/99	100	1.3
3ALC002.74	10/12/99	100	0.42
3ALC002.74	11/8/99	100	1.09
3ALC002.74	12/7/99	100	0.5
3ALC002.74	1/5/00	300	0.3
3ALC002.74	2/2/00	100	0.9
3ALC002.74	3/1/00	100	0.76
3ALC002.74	5/24/00	100	1.732
3ALC002.74	6/12/00	100	0

## **Appendix B – Bacteria Source Tracking Report**

The bacteria source tracking (BST) data were generated in a separate study performed by MapTech, Inc. The entire report from that study is included in this appendix, including Addendum A which contains data collected during the last four months of the study. The reader should refer to data and analyses for station 3DPR001.70.

## ADDENDUM A

**Table 1      Bacterial Enumeration - DEQ Phase 1 – September through December 2003.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3DPR001.70	9/9/2003	12:30 PM	9/10/2003	DM	9/18/2003	E. Coli	210	cfu/100 ml		
3DPR001.70	9/9/2003	12:30 PM	9/10/2003	DM	9/18/2003	Fecal Coliform	570	cfu/100 ml		
3DPR001.70	10/14/2003	2:40 PM	10/15/2003	DM	11/4/2003	E. Coli	5600	cfu/100 ml		
3DPR001.70	10/14/2003	2:40 PM	10/15/2003	DM	11/4/2003	Fecal Coliform	700	cfu/100 ml		
3DPR001.70	11/6/2003	3:20 PM	11/7/2003	DM	12/11/2003	E. Coli	1000	cfu/100 ml		
3DPR001.70	11/6/2003	3:20 PM	11/7/2003	DM	12/11/2003	Fecal Coliform	5000	cfu/100 ml		
3DPR001.70	12/16/2003	12:00 PM	12/17/2003	DM	1/20/2004	E. Coli	190	cfu/100 ml		
3DPR001.70	12/16/2003	12:00 PM	12/17/2003	DM	1/20/2004	Fecal Coliform	90	cfu/100 ml		
3MUU000.82	9/9/2003	11:05 AM	9/10/2003	DM	9/18/2003	E. Coli	140	cfu/100 ml		
3MUU000.82	9/9/2003	11:05 AM	9/10/2003	DM	9/18/2003	Fecal Coliform	400	cfu/100 ml		
3MUU000.82	10/14/2003	1:25 PM	10/15/2003	DM	11/4/2003	E. Coli	50	cfu/100 ml		
3MUU000.82	10/14/2003	1:25 PM	10/15/2003	DM	11/4/2003	Fecal Coliform	80	cfu/100 ml		
3MUU000.82	11/6/2003	1:55 PM	11/7/2003	DM	12/11/2003	E. Coli	1010	cfu/100 ml		
3MUU000.82	11/6/2003	1:55 PM	11/7/2003	DM	12/11/2003	Fecal Coliform	2900	cfu/100 ml		
3MUU000.82	12/16/2003	11:30 AM	12/17/2003	DM	1/20/2004	E. Coli	800	cfu/100 ml		
3MUU000.82	12/16/2003	11:30 AM	12/17/2003	DM	1/20/2004	Fecal Coliform	150	cfu/100 ml		
3MUU008.52	9/9/2003	11:45 AM	9/10/2003	DM	9/18/2003	E. Coli	740	cfu/100 ml		
3MUU008.52	9/9/2003	11:45 AM	9/10/2003	DM	9/18/2003	Fecal Coliform	3000	cfu/100 ml		
3MUU008.52	10/14/2003	1:50 PM	10/15/2003	DM	11/4/2003	E. Coli	660	cfu/100 ml		
3MUU008.52	10/14/2003	1:50 PM	10/15/2003	DM	11/4/2003	Fecal Coliform	300	cfu/100 ml		
3MUU008.52	11/6/2003	2:35 PM	11/7/2003	DM	12/11/2003	E. Coli	1300	cfu/100 ml		
3MUU008.52	11/6/2003	2:35 PM	11/7/2003	DM	12/11/2003	Fecal Coliform	6300	cfu/100 ml		
3MUU008.52	12/16/2003	11:00 AM	12/17/2003	DM	1/20/2004	E. Coli	250	cfu/100 ml		
3MUU008.52	12/16/2003	11:00 AM	12/17/2003	DM	1/20/2004	Fecal Coliform	1	cfu/100 ml	U	

**Table 2 Bacterial Source Tracking - DEQ Phase 1 – September through December 2003.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3DPR001.70	09/09/03	D1986	E10	24	210	<b>66%</b>	0%	<b>17%</b>	<b>17%</b>
3DPR001.70	10/14/03	D2228	E10	24	5600	<b>17%</b>	0%	<b>79%</b>	4%
3DPR001.70	11/06/03	D2417	E10	24	1000	<b>50%</b>	4%	<b>29%</b>	<b>17%</b>
3DPR001.70	12/16/03	D2668	E10	24	190	<b>54%</b>	<b>17%</b>	<b>25%</b>	4%
3MUU000.82	09/09/03	D1984	E07	24	140	<b>29%</b>	0%	<b>54%</b>	<b>17%</b>
3MUU000.82	10/14/03	D2226	E07	6	50	33%	17%	17%	33%
3MUU000.82	11/06/03	D2415	E07	24	1010	<b>54%</b>	0%	<b>38%</b>	8%
3MUU000.82	12/16/03	D2667	E07	24	800	<b>29%</b>	8%	<b>46%</b>	<b>17%</b>
3MUU008.52	09/09/03	D1985	E07	24	740	<b>46%</b>	0%	<b>33%</b>	<b>21%</b>
3MUU008.52	10/14/03	D2227	E07	24	660	<b>21%</b>	0%	<b>38%</b>	<b>41%</b>
3MUU008.52	11/06/03	D2416	E07	24	1300	<b>42%</b>	0%	<b>42%</b>	<b>16%</b>
3MUU008.52	12/16/03	D2666	E07	24	250	<b>54%</b>	0%	4%	<b>42%</b>

**BOLD** type indicates a statistically significant value.

# Bacterial Source Tracking Analyses to Support Virginia's TMDLs

## *Northern Region*

Prepared by  
**MapTech, Inc.**

in cooperation with

Virginia Polytechnic Institute and State University  
Crop and Soil Environmental Sciences Department

for

Virginia Department of Environmental Quality

Contract #19390-414321

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## **1. INTRODUCTION**

EPA's document, *Guidance for Water Quality-Based Decisions: The TMDL Process* (USEPA, 1999) states:

*According to section 303(d) of the Clean Water Act and EPA water quality planning and management regulations, States are required to identify waters that do not meet or are not expected to meet water quality standards even after technology-based or other required controls are in place. The water bodies are considered water quality-limited and require TMDLs.*

*. . . A TMDL, or total maximum daily load, is a tool for implementing State water quality standards and is based on the relationship between pollution sources and in-stream water quality conditions. The TMDL establishes the allowable loadings or other quantifiable parameters for a water body and thereby provides the basis for States to establish water quality-based controls. These controls should provide the pollution reduction necessary for a water body to meet water quality standards.*

The purpose of this project is to use bacterial source tracking to identify sources of *E. coli* to support the development of *E. coli* TMDLs for impaired segments in Virginia. In fulfilling the state requirement for the development of a TMDL, a systematic process will be utilized to establish the maximum allowable *E. coli* loading for each waterbody to meet the applicable standard, allocate that load among pollutant contributors, and provide a basis for taking actions needed to restore water quality.

Bacterial Source Tracking (BST) methods can be subdivided into three basic groups: Molecular, Biochemical, and Chemical. Molecular (genotype) are typically referred to as "DNA fingerprinting" and are based on the unique genetic makeup of different strains, or subspecies, of fecal bacteria. Biochemical (phenotype) methods are based on an effect of an organism's genes that actively produce a biochemical substance. The type and quantity of these substances produced is what is actually measured. Chemical methods are based on finding chemical compounds that are associated with human wastewaters, and generally are restricted to determining if sources of pollution are human or not.

Hagedorn's (Hagedorn et al., 1999) Antibiotic Resistance Analysis (ARA) technique was used for this project because it has been demonstrated to be a reliable procedure for confirming the presence of human, livestock, wildlife and pet sources. Compared to DNA fingerprinting, biochemical profiling is much quicker, typically allows for many more isolates to be analyzed (*e.g.*, hundreds per week vs. a few dozen per week for DNA analysis), is more economical, has survived limited court testing, and has undergone rigorous peer review from the scientific community. Additionally, observation of an increased number of isolates allows for an estimate of the relative proportions of the fecal indicator (*e.g.*, *E. coli*) originating from different sources.

## **2. OBJECTIVES**

BST was used to identify sources of *E. coli*, and the relative percentage contribution from four source groups (*i.e.*, livestock, wildlife, human and pets) to support the development of *E. coli* TMDLs for impairments located throughout Virginia. BST results will be used to improve public awareness of the problem, to improve model calibration/validation of *E. coli* densities and to provide a more equitable allocation of loads to source classes.

The specific objectives of the project were to:

1. collect fecal samples from known sources in 18 impairment areas, including the impairment area represented by the Appomattox River watershed;
2. use collected samples to develop a known-source library for each impairment area;  
and
3. perform bacterial enumerations and BST analyses on whole water samples from impaired segments, using the libraries developed for objective 2.

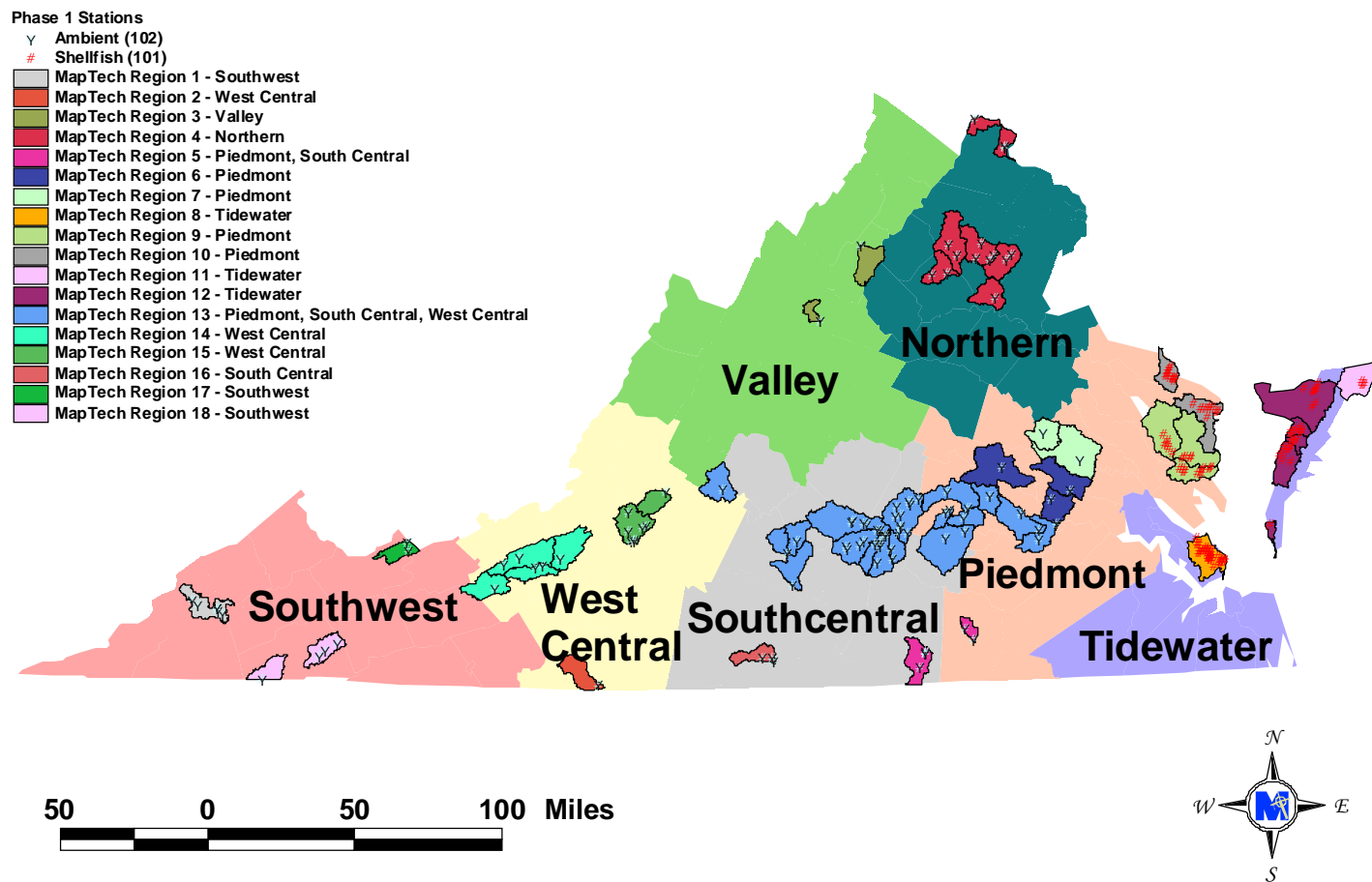
### **3. METHODS**

Hagedorn's ARA method has been extensively and successfully used by MapTech, and separates fecal sources based on patterns of antibiotic resistance in the *enterococci* or *E. coli*. For this study, *E. coli* was the indicator organism analyzed. The premise of ARA is that fecal bacteria from each source (*e.g.*, human, livestock, wildlife, and pets) will have different resistance patterns to the battery of antibiotics and concentrations used in the analysis. Hagedorn's method for *E. coli* tests each isolate on 28 different combinations of antibiotic type and concentration. Confidence in BST techniques is measured by the level of separation of isolates from known sources, represented as the percentage of isolates that are accurately separated into respective source types (*e.g.*, Average Rate of Correct Classification – ARCC). Additional analyses can be applied to test the specificity of the library. These analyses are discussed further in Section 4 of this document. The ARA method, like other methods (*e.g.*, molecular), requires the collection of source samples from feces of known sources to build a source library. Since source libraries had not been built for the study areas, known source samples from the four source classes were collected, analyzed, and entered into known-source libraries.

#### **3.1 Collection of Known Sources**

Known source samples were collected in eighteen regions associated with fecal-bacteria impaired waters throughout Virginia (Figure 3.1). Objective 1 was completed through the collection of 60 fecal samples from each of seventeen impairment areas (regions 1-12, 14-18) and collection of 160 fecal samples from impairment areas within the Appomattox River watershed (region 13). Each set of source samples was distributed evenly between human, livestock, wildlife, and pets (Table 3.1). Specific species within each source category (*e.g.*, deer, raccoon, poultry, beef, etc.) that were selected to represent the sources in each region were identified through field observation, discussion with local stakeholders, and review of available data (*e.g.*, Virginia Agricultural Statistics). From each sample, isolates were analyzed using BST to create a known-source library of 480 isolates for each region outside of the Appomattox River watershed, and 1,280 isolates for the Appomattox region. In total 1,180 fecal samples were collected for this study, resulting in 9,440 isolates analyzed.





**Figure 3.1** Spatial distribution of impaired segments identified within DEQ regions, and known-source library regions.

**Table 3.1 Source samples collected for BST library development.**

Source	Source Species	Number of Samples Collected in Each Region outside of the Appomattox Drainage	Number of Samples Collected within the Appomattox Drainage
Human	Septic Systems, Portable Toilets, ...	15	40
Livestock	Dairy, Beef, Horse, Sheep, Broilers, Turkeys, Swine, Waste Storage Pits, ...	15	40
Wildlife	Deer, Raccoon, Muskrat, Duck, Goose, ...	15	40
Pets	Dogs & Cats	15	40
Total		60	160

### **3.2 Development of Known-Source Libraries**

An appropriate known-source library was selected for each of the impairments to complete objective 2. A predictive model was developed from each library using logistic regression. A known-source library must be large enough to prevent an over-specified fit to the library. However, known-source responses to ARA analyses have been observed to vary geographically. The characteristics of this variance has not been well defined, so the regional libraries developed for this study were combined in a stepwise procedure and analyzed to measure the resulting specificity and the predictive accuracy of the combined libraries, as detailed in Section 4 of this document.

### **3.3 Bacterial Enumerations and BST Analyses**

For objective 3, water quality monitoring sites were identified and sampled by the granting agency (Tables 3.2 and 3.3). Although the contract began in August 2002, for many sites, sampling did not begin until later in the study. At the conclusion of the study, all sites will have been sampled monthly for one year. Samples were received either as whole-water samples (*i.e.*, ambient sampling as presented in Table 3.2) or filter plates (Table 3.3) from enumerations conducted on whole-water samples collected and analyzed by the Virginia Department of Health, Division of Shellfish Sanitation (VDH-DSS). All water samples were analyzed for *E. coli* and fecal coliform. BST was run on bacteria isolated from the whole-water samples or received on

plates from VDH-DSS. Bacteria were analyzed using Hagedorn's ARA methodology, yielding the percentage of isolates classified as human, livestock, wildlife, and pets. Up to 24 bacterial isolates were analyzed per sample, limited only by the number of isolates available from the enumeration process.

**Table 3.2      Distribution of ambient sampling stations addressed in this study (1 of 2).**

<b>Waterbody</b>	<b>Hydrologic Unit</b>	<b>BST Stations</b>
Piney Run	A01	1
Limestone Branch	A03	2
Licking Run	A17	2
Cedar Run	A18	4
Cub Run	B34	1
Hawksbill Creek	B39	1
Carter Run	E02	1
Great Run	E02	1
Muddy River	E07	1
Muddy Run	E07	1
Deep Run	E10	1
Mechumps Creek	F12	1
Matadequin Creek	F13	1
Fourmile Creek	G02	1
White Oak Swamp	G06	1
Reed Creek	H01	1
Tuckahoe Creek	H39	1
Looney Creek	I26	1
Horsepen Creek	J01	2
Vaughns Creek	J01	1
Mud Creek	J02	1
Spring Creek	J02	2
Buffalo Creek	J02	2
Little Sandy Creek	J03	2
Bush River	J04	3
Briery Creek	J05	2
Tanyard Branch	J05	1
Angola Creek	J06	2
Saylers Creek	J06	2
Little Saylers Creek	J06	2
Big Guinea Creek	J06	1
Flat Creek	J07	5
Nibbs Creek	J09	2
Deep Creek	J11	1
West Creek	J11	1
Appomattox River	J15	9
Swift Creek	J17	3
Roses Creek	K07	2
Wilsons Creek	L02	1
Carvin Creek	L05	1
Laymantown Creek	L05	1
Lick Run	L05	1
Tinker Creek	L05	2
Glade Creek	L05	2
Falling River, South Fork	L33	1
Falling River	L34	2
South Mayo River	L43	1
Birch Creek	L63	3
Unnamed Tributary to Flat Creek	L79	1

**Table 3.2**      **Distribution of ambient sampling stations addressed in this study (2 of 2).**

<b>Waterbody</b>	<b>Hydrologic Unit</b>	<b>BST Stations</b>
Peak Creek	N17	1
Crab Creek	N18	2
Bluestone River	N36	2
Hutton Creek	O05	1
Byers Creek	O05	1
Cedar Creek	O05	2
Beaver Creek	O07	1
Guest River	P11	1
Crab Orchard Branch	P11	1
Bear Creek	P11	1
Little Toms Creek	P11	1
Sepulcher Creek	P11	1
Toms Creek	P11	1

**Table 3.3      Distribution of stations sampled by VDH-DSS in support of this study.**

<b>Waterbody</b>	<b>Hydrologic Unit</b>	<b>BST Stations</b>
Yeocomico River	A33	9
W. Yeocomico River	A33	1
Lodge Creek	A33	1
Cockrell Creek	C01	2
Great Wicomico River	C01	6
Mill Creek to Dividing Creek	C01	1
Piankatank River: Healy Creek	C03	2
Upper Piankatank River	C03	4
Piankatank River: Wilton Creek	C03	1
Jackson Creek	C03	2
Lower Piankatank River	C03	1
White House Cove	C07	2
Poquoson River: Chisman Creek	C07	2
Easton Cove	C07	1
Patricks Creek	C07	1
Southwest Branch	C07	1
Poquoson River: Roberts Creek	C07	1
Bennett Creek	C07	1
Poquoson River	C07	3
Back River: Long & Gruland Creeks	C07	1
Harris River	C07	2
Back River: Front Cove	C07	1
Back River	C07	9
Lyons Creek	C07	1
Inlet	C07	1
Back Creek	C07	3
Lambs Creek	C07	1
Wallace Creek	C07	2
Young Creek	C10	1
Pocomoke Sound	C10	2
Messongo Creek	C10	4
Guilford Creek	C10	1
Matchotank Creek	C11	1
Onancock Creek	C11	2
Finneys Creek	C11	1
Onancock	C11	1
Taylor Creek	C12	1
Pungoteague Creek	C12	3
Occohannock Creek	C13	1
Craddock Creek	C13	2
Nandua Creek	C13	4
Old Plantation Creek	C16	1
Chincoteague Channel/Fowling Gut	D01	1
Assateague Channel	D01	2
Urbanna Creek	E25	1
Lagrange and Robinson	E25	3
Rappahannock River	E25	2
William Whiting and Meachim Creeks	E26	4

#### **4. KNOWN-SOURCE LIBRARY DEVELOPMENT**

As discussed in Section 3, a predictive model was developed from each library using logistic regression. The regional libraries developed for this study were combined in a stepwise procedure and analyzed to measure the resulting specificity and the predictive accuracy of the combined libraries. The specificity and predictive accuracy were assessed through three analyses. First, the ARCC was calculated for the library. Second, a randomization test was performed by randomly assigning source categories to samples and assessing the ARCC for the randomized library. Ten randomizations were performed and the results averaged. The expected result of randomization of four source categories is an ARCC of 25%, indicating a completely random result. Greater values for the randomized ARCC indicate a more specified model. Third, a jackknifing routine was conducted; where data from each whole fecal sample were individually withheld during development of the statistical model, then the model was tested for predictive accuracy on the withheld sample. In combining regional libraries a balance was sought between minimizing the randomized ARCC and maximizing the jackknifed ARCC. Table 4.1 shows the resulting analyses on the finalized libraries, and Table 4.2 shows the HUPs associated with each library.

**Table 4.1 Results of known-source library development.**

<b>Known-Source Library</b>	<b>Regional Libraries Included</b>	<b>ARCC (%)</b>	<b>Randomized ARCC (%)</b>	<b>Jackknifed ARCC (%)</b>
1	1, 17, 18	72	38	64
2	2, 14, 17	83	40	74
3	2, 14,15	76	39	63
4	13, 16	77	37	66
5	5,13	84	38	78
6	3, 4	90	41	79
7	6, 7, 13	70	35	60
8	8, 9	71	40	62
9	10, 12	67	43	52
10	11, 12	70	41	52

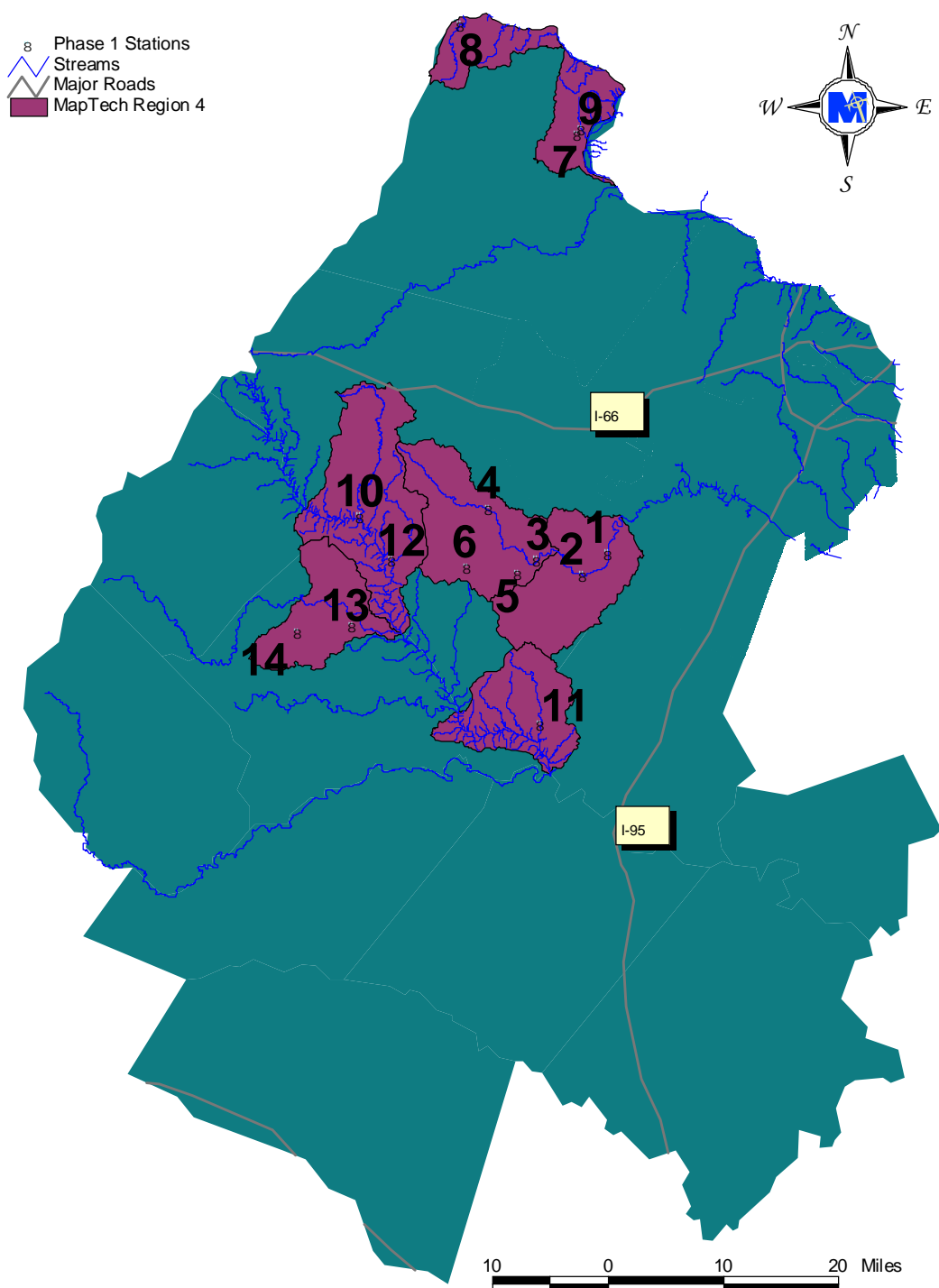
**Table 4.2 Known-source libraries associated with HUPs included in this study.**

<b>HUP</b>	<b>Known-Source Library</b>	<b>HUP</b>	<b>Known-Source Library</b>	<b>HUP</b>	<b>Known-Source Library</b>
A01	6	E25	8	J15	4
A03	6	E26	8	J16	4
A17	6	F12	7	J17	4
A18	6	F13	7	K07	5
A33	9	G02	7	L02	2
B34	6	G06	7	L05	3
B39	6	H01	3	L32	4
C01	9	H39	7	L33	4
C03	8	I26	3	L34	4
C07	8	J01	4	L43	2
C10	10	J02	4	L63	4
C11	10	J03	4	L79	5
C12	10	J04	4	N17	2
C13	10	J05	4	N18	2
C16	10	J06	4	N22	2
D01	10	J07	4	N36	2
E02	6	J09	4	O05	1
E07	6	J10	4	O07	1
E10	6	J11	4	P11	1



## **5. RESULTS**

The results of the water quality analyses for VADEQ's Northern Region (Figure 5.1) are reported in the following tables. Table 5.1 indicates the number of samples analyzed in the first year of sampling. As noted earlier, due to the beginning dates of sampling, not all stations have 12 months worth of data at the end of one year. Fecal coliform and *E. coli* enumerations are reported in Tables 5.2 through 5.15. The results of the BST analysis are reported in Tables 5.16 through 5.29. The *E. coli* enumerations are reported again here to give an indication of the bacteria concentration at the time of sampling. The proportions reported are formatted to indicate statistical significance (*i.e.*, **BOLD** numbers indicate a statistically significant result). The statistical significance was determined through 2 tests. The first was based on the sample size. A z-test was used to determine if the proportion was significantly different from zero ( $\alpha = 0.10$ ). Second the rate of false positives was calculated for each source category in each library, and a proportion was not considered significantly different from zero unless it was greater than the false-positive rate plus three standard deviations.



**Figure 5.1** Bacterial sampling stations in VADEQ's Northern Region.

**Table 5.1 Summary of bacterial sampling in VADEQ's Northern Region.**

Map ID	Station ID	HUP	County / City	Impairment	# of Samples Received	% Violations for <i>E. Coli</i>	% Violations for Fecal Coliform
1	1ACER006.00	A18	Prince William	Cedar Run	12	33%	42%
2	1ACER009.52	A18	Prince William	Cedar Run	12	50%	58%
3	1ACER016.46	A17	Fauquier	Cedar Run	12	42%	58%
4	1ACER025.25	A17	Fauquier	Cedar Run	12	50%	58%
5	1ALIL001.43	A17	Fauquier	Licking Run	12	42%	58%
6	1ALIL008.23	A17	Fauquier	Licking Run	8	25%	50%
7	1ALIM001.16	A03	Loudoun	Limestone Branch	12	42%	50%
8	1APIA001.80	A01	Loudoun	Piney Run	12	25%	50%
9	1AXAQ000.85	A03	Loudoun	Unnamed Tributary to Limestone Branch	12	67%	75%
10	3CAE000.25	E02	Fauquier	Carter Run	8	38%	50%
11	3DPR001.70	E10	Fauquier	Deep Run	8	38%	38%
12	3GRT001.70	E02	Fauquier	Great Run	7	14%	57%
13	3MUU000.82	E07	Culpeper	Muddy Run	7	57%	57%
14	3MUU008.52	E07	Culpeper	Muddy Run	8	63%	63%

**Table 5.2 Bacterial Enumeration for Cedar Run at Station 1ACER006.00.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ACER006.00	9/30/02	13:30	10/1/02	JJ	1/24/03	E. Coli	120	cfu/100 ml		
1ACER006.00	9/30/02	13:30	10/1/02	JJ	1/24/03	Fecal Coliform	300	cfu/100 ml		
1ACER006.00	10/17/02	13:30	10/18/02	JJ	1/24/03	E. Coli	22000	cfu/100 ml		
1ACER006.00	10/17/02	13:30	10/18/02	JJ	1/24/03	Fecal Coliform	60000	cfu/100 ml		
1ACER006.00	11/13/02	13:55	11/14/02	JJ	1/24/03	E. Coli	11000	cfu/100 ml		
1ACER006.00	11/13/02	13:55	11/14/02	JJ	1/24/03	Fecal Coliform	15000	cfu/100 ml		
1ACER006.00	12/16/02	14:25	12/17/02	JJ	1/24/03	E. Coli	260	cfu/100 ml		
1ACER006.00	12/16/02	14:25	12/17/02	JJ	1/24/03	Fecal Coliform	1000	cfu/100 ml		
1ACER006.00	1/29/03	15:15	1/30/03	JJ	2/21/03	E. Coli	1	cfu/100 ml	U	
1ACER006.00	1/29/03	15:15	1/30/03	JJ	2/21/03	Fecal Coliform	10	cfu/100 ml	U	
1ACER006.00	2/25/03	17:45	2/26/03	JJ	4/3/03	E. Coli	10	cfu/100 ml	U	Excessive sediment inhibited colony formation
1ACER006.00	2/25/03	17:45	2/26/03	JJ	4/3/03	Fecal Coliform	320	cfu/100 ml		Excessive sediment inhibited colony formation
1ACER006.00	3/4/03	14:45	3/5/03	JJ	4/3/03	E. Coli	94	cfu/100 ml		
1ACER006.00	3/4/03	14:45	3/5/03	JJ	4/3/03	Fecal Coliform	210	cfu/100 ml		
1ACER006.00	4/15/03	15:35	4/16/03	JJ	7/7/03	E. Coli	94	cfu/100 ml		
1ACER006.00	4/15/03	15:35	4/16/03	JJ	7/7/03	Fecal Coliform	100	cfu/100 ml		
1ACER006.00	5/12/03	15:00	5/13/03	JJ	7/7/03	E. Coli	270	cfu/100 ml		
1ACER006.00	5/12/03	15:00	5/13/03	JJ	7/7/03	Fecal Coliform	2300	cfu/100 ml		
1ACER006.00	6/25/03	14:30	6/26/03	JJ	7/7/03	E. Coli	130	cfu/100 ml		
1ACER006.00	6/25/03	14:30	6/26/03	JJ	7/7/03	Fecal Coliform	280	cfu/100 ml		
1ACER006.00	7/22/03	15:00	7/23/03	JJ	8/6/03	E. Coli	78	cfu/100 ml		
1ACER006.00	7/22/03	15:00	7/23/03	JJ	8/6/03	Fecal Coliform	260	cfu/100 ml		
1ACER006.00	8/18/03	14:45	8/19/03	JMc	9/18/03	E. Coli	62	cfu/100 ml		
1ACER006.00	8/18/03	14:45	8/19/03	JMc	9/18/03	Fecal Coliform	2500	cfu/100 ml		

**Table 5.3 Bacterial Enumeration for Cedar Run at station 1ACER009.52.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ACER009.52	8/27/02	15:47	8/28/02	JJ	1/24/03	E. Coli	1	cfu/100 ml	U	
1ACER009.52	8/27/02	15:47	8/28/02	JJ	1/24/03	Fecal Coliform	7100	cfu/100 ml		
1ACER009.52	9/30/02	13:00	10/1/02	JJ	1/24/03	E. Coli	14	cfu/100 ml		
1ACER009.52	9/30/02	13:00	10/1/02	JJ	1/24/03	Fecal Coliform	64	cfu/100 ml		
1ACER009.52	10/17/02	13:00	10/18/02	JJ	1/24/03	E. Coli	13000	cfu/100 ml		
1ACER009.52	10/17/02	13:00	10/18/02	JJ	1/24/03	Fecal Coliform	18000	cfu/100 ml		
1ACER009.52	11/13/02	13:25	11/14/02	JJ	1/24/03	E. Coli	10000	cfu/100 ml		
1ACER009.52	11/13/02	13:25	11/14/02	JJ	1/24/03	Fecal Coliform	12000	cfu/100 ml		
1ACER009.52	12/16/02	14:10	12/17/02	JJ	1/24/03	E. Coli	400	cfu/100 ml		
1ACER009.52	12/16/02	14:10	12/17/02	JJ	1/24/03	Fecal Coliform	900	cfu/100 ml		
1ACER009.52	1/29/03	14:50	1/30/03	JJ	2/21/03	E. Coli	1	cfu/100 ml	U	
1ACER009.52	1/29/03	14:50	1/30/03	JJ	2/21/03	Fecal Coliform	20	cfu/100 ml		
1ACER009.52	2/25/03	17:25	2/26/03	JJ	4/3/03	E. Coli	390	cfu/100 ml		
1ACER009.52	2/25/03	17:25	2/26/03	JJ	4/3/03	Fecal Coliform	570	cfu/100 ml		
1ACER009.52	3/4/03	14:25	3/5/03	JJ	4/3/03	E. Coli	72	cfu/100 ml		
1ACER009.52	3/4/03	14:25	3/5/03	JJ	4/3/03	Fecal Coliform	160	cfu/100 ml		
1ACER009.52	4/15/03	15:20	4/16/03	JJ	7/7/03	E. Coli	180	cfu/100 ml		
1ACER009.52	4/15/03	15:20	4/16/03	JJ	7/7/03	Fecal Coliform	210	cfu/100 ml		
1ACER009.52	5/12/03	14:40	5/13/03	JJ	7/7/03	E. Coli	520	cfu/100 ml		
1ACER009.52	5/12/03	14:40	5/13/03	JJ	7/7/03	Fecal Coliform	740	cfu/100 ml		
1ACER009.52	6/25/03	14:10	6/26/03	JJ	7/7/03	E. Coli	250	cfu/100 ml		
1ACER009.52	6/25/03	14:10	6/26/03	JJ	7/7/03	Fecal Coliform	480	cfu/100 ml		
1ACER009.52	7/22/03	14:40	7/23/03	JJ	8/6/03	E. Coli	88	cfu/100 ml		
1ACER009.52	7/22/03	14:40	7/23/03	JJ	8/6/03	Fecal Coliform	220	cfu/100 ml		

**Table 5.4 Bacterial Enumeration for Cedar Run at station 1ACER016.46.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ACER016.46	8/27/02	14:25	8/28/02	JJ	1/24/03	E. Coli	72	cfu/100 ml		
1ACER016.46	8/27/02	14:25	8/28/02	JJ	1/24/03	Fecal Coliform	1000	cfu/100 ml		
1ACER016.46	9/30/02	12:30	10/1/02	JJ	1/24/03	E. Coli	40	cfu/100 ml		
1ACER016.46	9/30/02	12:30	10/1/02	JJ	1/24/03	Fecal Coliform	100	cfu/100 ml		
1ACER016.46	10/17/02		10/18/02	JJ	1/24/03	E. Coli	81000	cfu/100 ml		
1ACER016.46	10/17/02		10/18/02	JJ	1/24/03	Fecal Coliform	95000	cfu/100 ml		
1ACER016.46	11/13/02	12:55	11/14/02	JJ	1/24/03	E. Coli	370	cfu/100 ml		
1ACER016.46	11/13/02	12:55	11/14/02	JJ	1/24/03	Fecal Coliform	3900	cfu/100 ml		
1ACER016.46	12/16/02	13:50	12/17/02	JJ	1/24/03	E. Coli	250	cfu/100 ml		
1ACER016.46	12/16/02	13:50	12/17/02	JJ	1/24/03	Fecal Coliform	740	cfu/100 ml		
1ACER016.46	1/29/03	14:20	1/30/03	JJ	2/21/03	E. Coli	1	cfu/100 ml	U	
1ACER016.46	1/29/03	14:20	1/30/03	JJ	2/21/03	Fecal Coliform	60	cfu/100 ml		
1ACER016.46	2/25/03	17:00	2/26/03	JJ	4/3/03	E. Coli	500	cfu/100 ml		
1ACER016.46	2/25/03	17:00	2/26/03	JJ	4/3/03	Fecal Coliform	800	cfu/100 ml		
1ACER016.46	3/4/03	14:05	3/5/03	JJ	4/3/03	E. Coli	88	cfu/100 ml		
1ACER016.46	3/4/03	14:05	3/5/03	JJ	4/3/03	Fecal Coliform	380	cfu/100 ml		
1ACER016.46	4/15/03	15:00	4/16/03	JJ	7/7/03	E. Coli	82	cfu/100 ml		
1ACER016.46	4/15/03	15:00	4/16/03	JJ	7/7/03	Fecal Coliform	170	cfu/100 ml		
1ACER016.46	5/12/03	14:20	5/13/03	JJ	7/7/03	E. Coli	990	cfu/100 ml		
1ACER016.46	5/12/03	14:20	5/13/03	JJ	7/7/03	Fecal Coliform	2000	cfu/100 ml		
1ACER016.46	6/25/03	13:50	6/26/03	JJ	7/7/03	E. Coli	140	cfu/100 ml		
1ACER016.46	6/25/03	13:50	6/26/03	JJ	7/7/03	Fecal Coliform	600	cfu/100 ml		
1ACER016.46	7/22/03	14:15	7/23/03	JJ	8/6/03	E. Coli	120	cfu/100 ml		
1ACER016.46	7/22/03	14:15	7/23/03	JJ	8/6/03	Fecal Coliform	200	cfu/100 ml		

**Table 5.5 Bacterial Enumeration for Cedar Run at station 1ACER025.25**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ACER025.25	8/27/02	14:00	8/28/02	JJ	1/24/03	E. Coli	21	cfu/100 ml		
1ACER025.25	8/27/02	14:00	8/28/02	JJ	1/24/03	Fecal Coliform	10000	cfu/100 ml		
1ACER025.25	9/30/02	11:30	10/1/02	JJ	1/24/03	E. Coli	220	cfu/100 ml		
1ACER025.25	9/30/02	11:30	10/1/02	JJ	1/24/03	Fecal Coliform	280	cfu/100 ml		
1ACER025.25	10/17/02	11:50	10/18/02	JJ	1/24/03	E. Coli	680	cfu/100 ml		
1ACER025.25	10/17/02	11:50	10/18/02	JJ	1/24/03	Fecal Coliform	2100	cfu/100 ml		
1ACER025.25	11/13/02	12:00	11/14/02	JJ	1/24/03	E. Coli	610	cfu/100 ml		
1ACER025.25	11/13/02	12:00	11/14/02	JJ	1/24/03	Fecal Coliform	13000	cfu/100 ml		
1ACER025.25	12/16/02	12:50	12/17/02	JJ	1/24/03	E. Coli	170	cfu/100 ml		
1ACER025.25	12/16/02	12:50	12/17/02	JJ	1/24/03	Fecal Coliform	400	cfu/100 ml		
1ACER025.25	2/25/03	15:55	2/26/03	JJ	4/3/03	E. Coli	2900	cfu/100 ml		
1ACER025.25	2/25/03	15:55	2/26/03	JJ	4/3/03	Fecal Coliform	3000	cfu/100 ml	L	
1ACER025.25	3/4/03	12:55	3/5/03	JJ	4/3/03	E. Coli	84	cfu/100 ml		
1ACER025.25	3/4/03	12:55	3/5/03	JJ	4/3/03	Fecal Coliform	230	cfu/100 ml		
1ACER025.25	4/15/03	13:55	4/16/03	JJ	7/7/03	E. Coli	27	cfu/100 ml		
1ACER025.25	4/15/03	13:55	4/16/03	JJ	7/7/03	Fecal Coliform	120	cfu/100 ml		
1ACER025.25	5/12/03	13:25	5/13/03	JJ	7/7/03	E. Coli	260	cfu/100 ml		
1ACER025.25	5/12/03	13:25	5/13/03	JJ	7/7/03	Fecal Coliform	490	cfu/100 ml		
1ACER025.25	6/25/03	12:40	6/26/03	JJ	7/7/03	E. Coli	140	cfu/100 ml		
1ACER025.25	6/25/03	12:40	6/26/03	JJ	7/7/03	Fecal Coliform	270	cfu/100 ml		
1ACER025.25	7/22/03	13:15	7/23/03	JJ	8/6/03	E. Coli	440	cfu/100 ml		
1ACER025.25	7/22/03	13:15	7/23/03	JJ	8/6/03	Fecal Coliform	3500	cfu/100 ml		
1ACER025.25	8/18/03	13:35	8/19/03	JMc	9/18/03	E. Coli	300	cfu/100 ml		
1ACER025.25	8/18/03	13:35	8/19/03	JMc	9/18/03	Fecal Coliform	2700	cfu/100 ml		

**Table 5.6 Bacterial Enumeration for Licking Run at station 1ALIL001.43.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ALIL001.43	8/27/02	14:46	8/28/02	JJ	1/24/03	E. Coli	170	cfu/100 ml	U	Excessive sediment inhibited colony formation Excessive sediment inhibited colony formation
1ALIL001.43	8/27/02	14:46	8/28/02	JJ	1/24/03	Fecal Coliform	12000	cfu/100 ml		
1ALIL001.43	9/30/02	12:10	10/1/02	JJ	1/24/03	E. Coli	25	cfu/100 ml		
1ALIL001.43	9/30/02	12:10	10/1/02	JJ	1/24/03	Fecal Coliform	200	cfu/100 ml		
1ALIL001.43	10/17/02	12:26	10/18/02	JJ	1/24/03	E. Coli	50000	cfu/100 ml		
1ALIL001.43	10/17/02	12:26	10/18/02	JJ	1/24/03	Fecal Coliform	60000	cfu/100 ml		
1ALIL001.43	11/13/02	12:40	11/14/02	JJ	1/24/03	E. Coli	350	cfu/100 ml		
1ALIL001.43	11/13/02	12:40	11/14/02	JJ	1/24/03	Fecal Coliform	4600	cfu/100 ml		
1ALIL001.43	12/16/02	13:30	12/17/02	JJ	1/24/03	E. Coli	360	cfu/100 ml		
1ALIL001.43	12/16/02	13:30	12/17/02	JJ	1/24/03	Fecal Coliform	500	cfu/100 ml		
1ALIL001.43	1/29/03	13:50	1/30/03	JJ	2/21/03	E. Coli	1	cfu/100 ml		
1ALIL001.43	1/29/03	13:50	1/30/03	JJ	2/21/03	Fecal Coliform	40	cfu/100 ml		
1ALIL001.43	2/25/03	16:40	2/26/03	JJ	4/3/03	E. Coli	67	cfu/100 ml		
1ALIL001.43	2/25/03	16:40	2/26/03	JJ	4/3/03	Fecal Coliform	600	cfu/100 ml		
1ALIL001.43	3/4/03	13:45	3/5/03	JJ	4/3/03	E. Coli	130	cfu/100 ml		
1ALIL001.43	3/4/03	13:45	3/5/03	JJ	4/3/03	Fecal Coliform	160	cfu/100 ml		
1ALIL001.43	4/15/03	14:40	4/16/03	JJ	7/7/03	E. Coli	86	cfu/100 ml		
1ALIL001.43	4/15/03	14:40	4/16/03	JJ	7/7/03	Fecal Coliform	100	cfu/100 ml		
1ALIL001.43	5/12/03	14:05	5/13/03	JJ	7/7/03	E. Coli	410	cfu/100 ml		
1ALIL001.43	5/12/03	14:05	5/13/03	JJ	7/7/03	Fecal Coliform	800	cfu/100 ml		
1ALIL001.43	6/25/03	13:35	6/26/03	JJ	7/7/03	E. Coli	380	cfu/100 ml		
1ALIL001.43	6/25/03	13:35	6/26/03	JJ	7/7/03	Fecal Coliform	520	cfu/100 ml		
1ALIL001.43	7/22/03	13:55	7/23/03	JJ	8/6/03	E. Coli	94	cfu/100 ml		
1ALIL001.43	7/22/03	13:55	7/23/03	JJ	8/6/03	Fecal Coliform	210	cfu/100 ml		



**Table 5.7 Bacterial Enumeration for Licking Run at station 1ALIL008.23.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ALIL008.23	12/16/02	13:10	12/17/02	JJ	1/24/03	E. Coli	170	cfu/100 ml		
1ALIL008.23	12/16/02	13:10	12/17/02	JJ	1/24/03	Fecal Coliform	560	cfu/100 ml		
1ALIL008.23	2/25/03	16:15	2/26/03	JJ	4/3/03	E. Coli	18	cfu/100 ml		
1ALIL008.23	2/25/03	16:15	2/26/03	JJ	4/3/03	Fecal Coliform	210	cfu/100 ml		
1ALIL008.23	3/4/03	13:15	3/5/03	JJ	4/3/03	E. Coli	22	cfu/100 ml		
1ALIL008.23	3/4/03	13:15	3/5/03	JJ	4/3/03	Fecal Coliform	40	cfu/100 ml		
1ALIL008.23	4/15/03	14:20	4/16/03	JJ	7/7/03	E. Coli	150	cfu/100 ml		
1ALIL008.23	4/15/03	14:20	4/16/03	JJ	7/7/03	Fecal Coliform	180	cfu/100 ml		
1ALIL008.23	5/12/03	13:45	5/13/03	JJ	7/7/03	E. Coli	200	cfu/100 ml		
1ALIL008.23	5/12/03	13:45	5/13/03	JJ	7/7/03	Fecal Coliform	390	cfu/100 ml		
1ALIL008.23	6/25/03	13:15	6/26/03	JJ	7/7/03	E. Coli	460	cfu/100 ml		
1ALIL008.23	6/25/03	13:15	6/26/03	JJ	7/7/03	Fecal Coliform	2000	cfu/100 ml		
1ALIL008.23	7/22/03	13:35	7/23/03	JJ	8/6/03	E. Coli	620	cfu/100 ml		
1ALIL008.23	7/22/03	13:35	7/23/03	JJ	8/6/03	Fecal Coliform	2000	cfu/100 ml		
1ALIL008.23	8/18/03	13:55	8/19/03	JMc	9/18/03	E. Coli	150	cfu/100 ml		
1ALIL008.23	8/18/03	13:55	8/19/03	JMc	9/18/03	Fecal Coliform	3500	cfu/100 ml		

**Table 5.8 Bacterial Enumeration for Limestone Branch at station 1ALIM001.16.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1ALIM001.16	8/27/02	11:07	8/28/02	JJ	1/24/03	E. Coli	220	cfu/100 ml		
1ALIM001.16	8/27/02	11:07	8/28/02	JJ	1/24/03	Fecal Coliform	1100	cfu/100 ml		
1ALIM001.16	9/30/02	10:30	10/1/02	JJ	1/24/03	E. Coli	580	cfu/100 ml		
1ALIM001.16	9/30/02	10:30	10/1/02	JJ	1/24/03	Fecal Coliform	1500	cfu/100 ml		
1ALIM001.16	10/17/02	10:40	10/18/02	JJ	1/24/03	E. Coli	1100	cfu/100 ml		
1ALIM001.16	10/17/02	10:40	10/18/02	JJ	1/24/03	Fecal Coliform	5000	cfu/100 ml		
1ALIM001.16	11/13/02	11:00	11/14/02	JJ	1/24/03	E. Coli	110	cfu/100 ml		
1ALIM001.16	11/13/02	11:00	11/14/02	JJ	1/24/03	Fecal Coliform	220	cfu/100 ml		
1ALIM001.16	12/16/02	9:40	12/17/02	JJ	1/24/03	E. Coli	90	cfu/100 ml		
1ALIM001.16	12/16/02	9:40	12/17/02	JJ	1/24/03	Fecal Coliform	210	cfu/100 ml		
1ALIM001.16	1/29/03	11:30	1/30/03	JJ	2/21/03	E. Coli	34	cfu/100 ml		
1ALIM001.16	1/29/03	11:30	1/30/03	JJ	2/21/03	Fecal Coliform	80	cfu/100 ml		
1ALIM001.16	2/25/03	14:30	2/26/03	JJ	4/3/03	E. Coli	68	cfu/100 ml		
1ALIM001.16	2/25/03	14:30	2/26/03	JJ	4/3/03	Fecal Coliform	170	cfu/100 ml		
1ALIM001.16	3/4/03	11:15	3/5/03	JJ	4/3/03	E. Coli	28	cfu/100 ml		
1ALIM001.16	3/4/03	11:15	3/5/03	JJ	4/3/03	Fecal Coliform	80	cfu/100 ml		
1ALIM001.16	4/15/03	12:40	4/16/03	JJ	7/7/03	E. Coli	80	cfu/100 ml		
1ALIM001.16	4/15/03	12:40	4/16/03	JJ	7/7/03	Fecal Coliform	140	cfu/100 ml		
1ALIM001.16	5/12/03	12:00	5/13/03	JJ	7/7/03	E. Coli	260	cfu/100 ml		
1ALIM001.16	5/12/03	12:00	5/13/03	JJ	7/7/03	Fecal Coliform	680	cfu/100 ml		
1ALIM001.16	6/25/03	11:30	6/26/03	JJ	7/7/03	E. Coli	500	cfu/100 ml		
1ALIM001.16	6/25/03	11:30	6/26/03	JJ	7/7/03	Fecal Coliform	670	cfu/100 ml		
1ALIM001.16	7/22/03	11:45	7/23/03	JJ	8/6/03	E. Coli	510	cfu/100 ml		
1ALIM001.16	7/22/03	11:45	7/23/03	JJ	8/6/03	Fecal Coliform	850	cfu/100 ml		

**Table 5.9 Bacterial Enumeration for Limestone Branch at station 1AXAQ000.85.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1AXAQ000.85	8/27/02	11:15	8/28/02	JJ	1/24/03	E. Coli	140	cfu/100 ml		
1AXAQ000.85	8/27/02	11:15	8/28/02	JJ	1/24/03	Fecal Coliform	16000	cfu/100 ml		
1AXAQ000.85	9/30/02	10:20	10/1/02	JJ	1/24/03	E. Coli	370	cfu/100 ml		
1AXAQ000.85	9/30/02	10:20	10/1/02	JJ	1/24/03	Fecal Coliform	1000	cfu/100 ml		
1AXAQ000.85	10/17/02	10:30	10/18/02	JJ	1/24/03	E. Coli	1500	cfu/100 ml		
1AXAQ000.85	10/17/02	10:30	10/18/02	JJ	1/24/03	Fecal Coliform	10000	cfu/100 ml		
1AXAQ000.85	11/13/02	10:45	11/14/02	JJ	1/24/03	E. Coli	890	cfu/100 ml		
1AXAQ000.85	11/13/02	10:45	11/14/02	JJ	1/24/03	Fecal Coliform	2000	cfu/100 ml		
1AXAQ000.85	12/16/02	9:50	12/17/02	JJ	1/24/03	E. Coli	360	cfu/100 ml		
1AXAQ000.85	12/16/02	9:50	12/17/02	JJ	1/24/03	Fecal Coliform	780	cfu/100 ml		
1AXAQ000.85	1/29/03	11:15	1/30/03	JJ	2/21/03	E. Coli	56	cfu/100 ml		
1AXAQ000.85	1/29/03	11:15	1/30/03	JJ	2/21/03	Fecal Coliform	130	cfu/100 ml		
1AXAQ000.85	2/25/03	14:20	2/26/03	JJ	4/3/03	E. Coli	680	cfu/100 ml		
1AXAQ000.85	2/25/03	14:20	2/26/03	JJ	4/3/03	Fecal Coliform	700	cfu/100 ml		
1AXAQ000.85	3/4/03	11:00	3/5/03	JJ	4/3/03	E. Coli	60	cfu/100 ml		
1AXAQ000.85	3/4/03	11:00	3/5/03	JJ	4/3/03	Fecal Coliform	200	cfu/100 ml		
1AXAQ000.85	4/15/03	12:25	4/16/03	JJ	7/7/03	E. Coli	110	cfu/100 ml		
1AXAQ000.85	4/15/03	12:25	4/16/03	JJ	7/7/03	Fecal Coliform	200	cfu/100 ml		
1AXAQ000.85	5/12/03	11:50	5/13/03	JJ	7/7/03	E. Coli	530	cfu/100 ml		
1AXAQ000.85	5/12/03	11:50	5/13/03	JJ	7/7/03	Fecal Coliform	2600	cfu/100 ml		
1AXAQ000.85	6/25/03	11:20	6/26/03	JJ	7/7/03	E. Coli	1400	cfu/100 ml		
1AXAQ000.85	6/25/03	11:20	6/26/03	JJ	7/7/03	Fecal Coliform	4200	cfu/100 ml		
1AXAQ000.85	7/22/03	11:35	7/23/03	JJ	8/6/03	E. Coli	1100	cfu/100 ml		
1AXAQ000.85	7/22/03	11:35	7/23/03	JJ	8/6/03	Fecal Coliform	2900	cfu/100 ml		

**Table 5.10 Bacterial Enumeration for Piney Run at station 1APIA001.80.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
1APIA001.80	8/27/02	12:10	8/28/02	JJ	1/24/03	E. Coli	110	cfu/100 ml		
1APIA001.80	8/27/02	12:10	8/28/02	JJ	1/24/03	Fecal Coliform	4600	cfu/100 ml		
1APIA001.80	9/30/02	9:40	10/1/02	JJ	1/24/03	E. Coli	200	cfu/100 ml		
1APIA001.80	9/30/02	9:40	10/1/02	JJ	1/24/03	Fecal Coliform	630	cfu/100 ml		
1APIA001.80	10/17/02	9:45	10/18/02	JJ	1/24/03	E. Coli	960	cfu/100 ml		
1APIA001.80	10/17/02	9:45	10/18/02	JJ	1/24/03	Fecal Coliform	3000	cfu/100 ml		
1APIA001.80	11/13/02	10:00	11/14/02	JJ	1/24/03	E. Coli	190	cfu/100 ml		
1APIA001.80	11/13/02	10:00	11/14/02	JJ	1/24/03	Fecal Coliform	400	cfu/100 ml		
1APIA001.80	12/16/02	10:40	12/17/02	JJ	1/24/03	E. Coli	100	cfu/100 ml		
1APIA001.80	12/16/02	10:40	12/17/02	JJ	1/24/03	Fecal Coliform	280	cfu/100 ml		
1APIA001.80	2/25/03	13:25	2/26/03	JJ	4/3/03	E. Coli	64	cfu/100 ml		
1APIA001.80	2/25/03	13:25	2/26/03	JJ	4/3/03	Fecal Coliform	300	cfu/100 ml		
1APIA001.80	3/4/03	10:05	3/5/03	JJ	4/3/03	E. Coli	64	cfu/100 ml		
1APIA001.80	3/4/03	10:05	3/5/03	JJ	4/3/03	Fecal Coliform	170	cfu/100 ml		
1APIA001.80	4/15/03	11:35	4/16/03	JJ	7/7/03	E. Coli	90	cfu/100 ml		
1APIA001.80	4/15/03	11:35	4/16/03	JJ	7/7/03	Fecal Coliform	110	cfu/100 ml		
1APIA001.80	5/12/03	10:55	5/13/03	JJ	7/7/03	E. Coli	120	cfu/100 ml		
1APIA001.80	5/12/03	10:55	5/13/03	JJ	7/7/03	Fecal Coliform	270	cfu/100 ml		
1APIA001.80	6/25/03	10:20	6/26/03	JJ	7/7/03	E. Coli	120	cfu/100 ml		
1APIA001.80	6/25/03	10:20	6/26/03	JJ	7/7/03	Fecal Coliform	800	cfu/100 ml		
1APIA001.80	7/22/03	10:45	7/23/03	JJ	8/6/03	E. Coli	460	cfu/100 ml		
1APIA001.80	7/22/03	10:45	7/23/03	JJ	8/6/03	Fecal Coliform	590	cfu/100 ml		
1APIA001.80	8/18/03	11:45	8/19/03	JMc	9/18/03	E. Coli	410	cfu/100 ml		
1APIA001.80	8/18/03	11:45	8/19/03	JMc	9/18/03	Fecal Coliform	2000	cfu/100 ml		

**Table 5.11 Bacterial Enumeration for Carter Run at station 3CAE000.25.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3CAE000.25	12/17/02	10:40	12/18/02	JJ	1/24/03	E. Coli	190	cfu/100 ml		
3CAE000.25	12/17/02	10:40	12/18/02	JJ	1/24/03	Fecal Coliform	300	cfu/100 ml		
3CAE000.25	1/28/03	10:30	1/29/03	JJ	2/21/03	E. Coli	22	cfu/100 ml		
3CAE000.25	1/28/03	10:30	1/29/03	JJ	2/21/03	Fecal Coliform	50	cfu/100 ml		
3CAE000.25	3/5/03	9:50	3/6/03	JJ	4/3/03	E. Coli	200	cfu/100 ml		
3CAE000.25	3/5/03	9:50	3/6/03	JJ	4/3/03	Fecal Coliform	220	cfu/100 ml		
3CAE000.25	4/16/03	11:55	4/17/03	JJ	7/7/03	E. Coli	200	cfu/100 ml		
3CAE000.25	4/16/03	11:55	4/17/03	JJ	7/7/03	Fecal Coliform	400	cfu/100 ml		
3CAE000.25	5/20/03	9:45	5/21/03	JJ	7/7/03	E. Coli	310	cfu/100 ml		
3CAE000.25	5/20/03	9:45	5/21/03	JJ	7/7/03	Fecal Coliform	600	cfu/100 ml		
3CAE000.25	6/23/03	11:35	6/24/03	JJ	7/7/03	E. Coli	290	cfu/100 ml		
3CAE000.25	6/23/03	11:35	6/24/03	JJ	7/7/03	Fecal Coliform	4200	cfu/100 ml		
3CAE000.25	7/21/03	10:35	7/22/03	JJ	8/6/03	E. Coli	390	cfu/100 ml		
3CAE000.25	7/21/03	10:35	7/22/03	JJ	8/6/03	Fecal Coliform	3200	cfu/100 ml		
3CAE000.25	8/19/03	10:35	8/20/03	JMc	9/18/03	E. Coli	160	cfu/100 ml		
3CAE000.25	8/19/03	10:35	8/20/03	JMc	9/18/03	Fecal Coliform	530	cfu/100 ml		

**Table 5.12 Bacterial Enumeration for Deep Run at Station 3DPR001.70.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3DPR001.70	12/17/02	13:10	12/18/02	JJ	1/24/03	E. Coli	35	cfu/100 ml		
3DPR001.70	12/17/02	13:10	12/18/02	JJ	1/24/03	Fecal Coliform	50	cfu/100 ml		
3DPR001.70	1/28/03	13:30	1/29/03	JJ	2/21/03	E. Coli	15	cfu/100 ml		
3DPR001.70	1/28/03	13:30	1/29/03	JJ	2/21/03	Fecal Coliform	40	cfu/100 ml		
3DPR001.70	3/5/03	12:40	3/6/03	JJ	4/3/03	E. Coli	44	cfu/100 ml		
3DPR001.70	3/5/03	12:40	3/6/03	JJ	4/3/03	Fecal Coliform	70	cfu/100 ml		
3DPR001.70	4/16/03	14:05	4/17/03	JJ	7/7/03	E. Coli	250	cfu/100 ml		
3DPR001.70	4/16/03	14:05	4/17/03	JJ	7/7/03	Fecal Coliform	380	cfu/100 ml		
3DPR001.70	5/20/03	12:50	5/21/03	JJ	7/7/03	E. Coli	160	cfu/100 ml		
3DPR001.70	5/20/03	12:50	5/21/03	JJ	7/7/03	Fecal Coliform	210	cfu/100 ml		
3DPR001.70	6/23/03	14:25	6/24/03	JJ	7/7/03	E. Coli	210	cfu/100 ml		
3DPR001.70	6/23/03	14:25	6/24/03	JJ	7/7/03	Fecal Coliform	460	cfu/100 ml		
3DPR001.70	7/21/03	13:55	7/22/03	JJ	8/6/03	E. Coli	400	cfu/100 ml		
3DPR001.70	7/21/03	13:55	7/22/03	JJ	8/6/03	Fecal Coliform	2000	cfu/100 ml		
3DPR001.70	8/19/03	13:45	8/20/03	JMc	9/18/03	E. Coli	720	cfu/100 ml		
3DPR001.70	8/19/03	13:45	8/20/03	JMc	9/18/03	Fecal Coliform	3000	cfu/100 ml		

**Table 5.13 Bacterial Enumeration for Great Run at Station 3GRT001.70.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3GRT001.70	12/17/02	11:25	12/18/02	JJ	1/24/03	E. Coli	70	cfu/100 ml		
3GRT001.70	12/17/02	11:25	12/18/02	JJ	1/24/03	Fecal Coliform	270	cfu/100 ml		
3GRT001.70	3/5/03	10:35	3/6/03	JJ	4/3/03	E. Coli	60	cfu/100 ml		
3GRT001.70	3/5/03	10:35	3/6/03	JJ	4/3/03	Fecal Coliform	80	cfu/100 ml		
3GRT001.70	4/16/03	11:55	4/17/03	JJ	7/7/03	E. Coli	78	cfu/100 ml		
3GRT001.70	4/16/03	11:55	4/17/03	JJ	7/7/03	Fecal Coliform	100	cfu/100 ml		
3GRT001.70	5/20/03	10:35	5/21/03	JJ	7/7/03	E. Coli	410	cfu/100 ml		
3GRT001.70	5/20/03	10:35	5/21/03	JJ	7/7/03	Fecal Coliform	650	cfu/100 ml		
3GRT001.70	6/23/03	12:15	6/24/03	JJ	7/7/03	E. Coli	140	cfu/100 ml		
3GRT001.70	6/23/03	12:15	6/24/03	JJ	7/7/03	Fecal Coliform	550	cfu/100 ml		
3GRT001.70	7/21/03	11:20	7/22/03	JJ	8/6/03	E. Coli	230	cfu/100 ml		
3GRT001.70	7/21/03	11:20	7/22/03	JJ	8/6/03	Fecal Coliform	500	cfu/100 ml		
3GRT001.70	8/19/03	11:15	8/20/03	JMc	9/18/03	E. Coli	170	cfu/100 ml		
3GRT001.70	8/19/03	11:15	8/20/03	JMc	9/18/03	Fecal Coliform	490	cfu/100 ml		

**Table 5.14 Bacterial Enumeration for Muddy Run at Station 3MUU000.82.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3MUU000.82	12/17/02	11:45	12/18/02	JJ	1/24/03	E. Coli	100	cfu/100 ml		
3MUU000.82	12/17/02	11:45	12/18/02	JJ	1/24/03	Fecal Coliform	250	cfu/100 ml		
3MUU000.82	3/5/03	11:05	3/6/03	JJ	4/3/03	E. Coli	120	cfu/100 ml		
3MUU000.82	3/5/03	11:05	3/6/03	JJ	4/3/03	Fecal Coliform	140	cfu/100 ml		
3MUU000.82	4/16/03	12:30	4/17/03	JJ	7/7/03	E. Coli	260	cfu/100 ml		
3MUU000.82	4/16/03	12:30	4/17/03	JJ	7/7/03	Fecal Coliform	300	cfu/100 ml		
3MUU000.82	5/20/03	11:05	5/21/03	JJ	7/7/03	E. Coli	680	cfu/100 ml		
3MUU000.82	5/20/03	11:05	5/21/03	JJ	7/7/03	Fecal Coliform	810	cfu/100 ml		
3MUU000.82	6/23/03	12:50	6/24/03	JJ	7/7/03	E. Coli	240	cfu/100 ml		
3MUU000.82	6/23/03	12:50	6/24/03	JJ	7/7/03	Fecal Coliform	800	cfu/100 ml		
3MUU000.82	7/21/03	12:30	7/22/03	JJ	8/6/03	E. Coli	310	cfu/100 ml		
3MUU000.82	7/21/03	12:30	7/22/03	JJ	8/6/03	Fecal Coliform	600	cfu/100 ml		
3MUU000.82	8/19/03	11:55	8/20/03	JMc	9/18/03	E. Coli	100	cfu/100 ml		
3MUU000.82	8/19/03	11:55	8/20/03	JMc	9/18/03	Fecal Coliform	590	cfu/100 ml		



**Table 5.15 Bacterial Enumeration for Muddy Run at Station 3MUU008.52.**

VADEQ ID	Date of Sample	Time of Sample	Analyte Received Date	Chemist Name	Sign Date	Constituent	Value	Units	Quality	Laboratory Comments
3MUU008.52	12/17/02	12:20	12/18/02	JJ	1/24/03	E. Coli	150	cfu/100 ml		
3MUU008.52	12/17/02	12:20	12/18/02	JJ	1/24/03	Fecal Coliform	200	cfu/100 ml		
3MUU008.52	1/28/03	12:30	1/29/03	JJ	2/21/03	E. Coli	12	cfu/100 ml		
3MUU008.52	1/28/03	12:30	1/29/03	JJ	2/21/03	Fecal Coliform	40	cfu/100 ml		
3MUU008.52	3/5/03	11:45	3/6/03	JJ	4/3/03	E. Coli	60	cfu/100 ml		
3MUU008.52	3/5/03	11:45	3/6/03	JJ	4/3/03	Fecal Coliform	110	cfu/100 ml		
3MUU008.52	4/16/03	13:10	4/17/03	JJ	7/7/03	E. Coli	700	cfu/100 ml		
3MUU008.52	4/16/03	13:10	4/17/03	JJ	7/7/03	Fecal Coliform	1900	cfu/100 ml		
3MUU008.52	5/20/03	12:00	5/21/03	JJ	7/7/03	E. Coli	1700	cfu/100 ml		
3MUU008.52	5/20/03	12:00	5/21/03	JJ	7/7/03	Fecal Coliform	2600	cfu/100 ml		
3MUU008.52	6/23/03	13:35	6/24/03	JJ	7/7/03	E. Coli	610	cfu/100 ml		
3MUU008.52	6/23/03	13:35	6/24/03	JJ	7/7/03	Fecal Coliform	700	cfu/100 ml		
3MUU008.52	7/21/03	13:10	7/22/03	JJ	8/6/03	E. Coli	1800	cfu/100 ml		
3MUU008.52	7/21/03	13:10	7/22/03	JJ	8/6/03	Fecal Coliform	7900	cfu/100 ml		
3MUU008.52	8/19/03	12:50	8/20/03	JMc	9/18/03	E. Coli	1500	cfu/100 ml		
3MUU008.52	8/19/03	12:50	8/20/03	JMc	9/18/03	Fecal Coliform	6300	cfu/100 ml		

Table 5.16 Bacterial Source Tracking for Cedar Run at Station 1ACER006.00.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ACER006.00	09/30/2002	D37	A18	21	120	<b>34%</b>	<b>33%</b>	<b>33%</b>	0%
1ACER006.00	10/17/2002	D69	A18	24	22,000	<b>37%</b>	<b>33%</b>	<b>17%</b>	<b>13%</b>
1ACER006.00	11/13/2002	D147	A18	24	11,000	<b>13%</b>	4%	<b>45%</b>	<b>38%</b>
1ACER006.00	12/16/2002	D333	A18	24	260	<b>50%</b>	4%	<b>25%</b>	<b>21%</b>
1ACER006.00	01/29/2003	D573	A18	0	<1	--	--	--	--
1ACER006.00	02/25/2003	D728	A18	0	<10	--	--	--	--
1ACER006.00	03/04/2003	D750	A18	24	94	8%	4%	<b>50%</b>	<b>38%</b>
1ACER006.00	04/15/2003	D979	A18	24	94	<b>33%</b>	4%	13%	<b>50%</b>
1ACER006.00	05/12/2003	D1105	A18	24	270	8%	8%	4%	<b>80%</b>
1ACER006.00	06/25/2003	D1399	A18	24	130	<b>63%</b>	<b>21%</b>	8%	8%
1ACER006.00	07/22/2003	D1622	A18	24	78	<b>38%</b>	4%	<b>38%</b>	<b>20%</b>
1ACER006.00	08/18/2003	D1820	A18	24	62	8%	0%	4%	<b>88%</b>

**BOLD** type indicates a statistically significant value.

Table 5.17 Bacterial Source Tracking for Cedar Run at Station 1ACER009.52.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ACER009.52	08/27/2002	D7	A18	16	<1	--	--	--	--
1ACER009.52	09/30/2002	D36	A18	7	14	72%	14%	14%	0%
1ACER009.52	10/17/2002	D68	A18	24	13,000	<b>58%</b>	4%	13%	<b>25%</b>
1ACER009.52	11/13/2002	D146	A18	24	10,000	<b>21%</b>	<b>21%</b>	<b>33%</b>	<b>25%</b>
1ACER009.52	12/16/2002	D332	A18	24	400	0%	0%	8%	<b>92%</b>
1ACER009.52	01/29/2003	D572	A18	0	<1	--	--	--	--
1ACER009.52	02/25/2003	D727	A18	24	390	4%	0%	<b>83%</b>	<b>13%</b>
1ACER009.52	03/04/2003	D749	A18	24	72	<b>21%</b>	4%	<b>17%</b>	<b>58%</b>
1ACER009.52	04/15/2003	D978	A18	24	180	<b>29%</b>	0%	13%	<b>58%</b>
1ACER009.52	05/12/2003	D1104	A18	24	520	<b>29%</b>	4%	<b>29%</b>	<b>38%</b>
1ACER009.52	06/25/2003	D1398	A18	24	250	<b>80%</b>	8%	8%	4%
1ACER009.52	07/22/2003	D1621	A18	24	88	<b>41%</b>	8%	13%	<b>38%</b>

**BOLD** type indicates a statistically significant value.

Table 5.18 Bacterial Source Tracking for Cedar Run at Station 1ACER016.46.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ACER016.46	08/27/2002	D5	A17	24	72	<b>17%</b>	<b>46%</b>	4%	<b>33%</b>
1ACER016.46	09/30/2002	D35	A17	24	40	<b>29%</b>	<b>38%</b>	<b>33%</b>	0%
1ACER016.46	10/17/2002	D62	A17	24	81,000	<b>29%</b>	8%	<b>29%</b>	<b>34%</b>
1ACER016.46	11/13/2002	D145	A17	24	370	<b>38%</b>	0%	<b>62%</b>	0%
1ACER016.46	12/16/2002	D331	A17	24	250	<b>13%</b>	0%	4%	<b>83%</b>
1ACER016.46	01/29/2003	D571	A17	0	<1	--	--	--	--
1ACER016.46	02/25/2003	D726	A17	24	500	<b>13%</b>	0%	<b>79%</b>	8%
1ACER016.46	03/04/2003	D748	A17	24	88	8%	0%	<b>33%</b>	<b>59%</b>
1ACER016.46	04/15/2003	D977	A17	24	82	<b>13%</b>	8%	<b>21%</b>	<b>58%</b>
1ACER016.46	05/12/2003	D1103	A17	24	990	<b>29%</b>	<b>17%</b>	8%	<b>46%</b>
1ACER016.46	06/25/2003	D1397	A17	24	140	<b>25%</b>	8%	<b>21%</b>	<b>46%</b>
1ACER016.46	07/22/2003	D1620	A17	24	120	<b>38%</b>	8%	<b>21%</b>	<b>33%</b>

**BOLD** type indicates a statistically significant value.

Table 5.19 Bacterial Source Tracking for Cedar Run at Station 1ACER025.25.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ACER025.25	08/27/2002	D4	A17	24	21	<b>61%</b>	<b>13%</b>	13%	<b>13%</b>
1ACER025.25	09/30/2002	D33	A17	24	220	<b>17%</b>	<b>75%</b>	8%	0%
1ACER025.25	10/17/2002	D66	A17	24	680	<b>33%</b>	<b>13%</b>	<b>29%</b>	<b>25%</b>
1ACER025.25	11/13/2002	D143	A17	24	610	<b>58%</b>	0%	<b>42%</b>	0%
1ACER025.25	12/16/2002	D328	A17	24	170	8%	4%	<b>25%</b>	<b>63%</b>
1ACER025.25	02/25/2003	D723	A17	24	2,900	8%	<b>13%</b>	<b>66%</b>	<b>13%</b>
1ACER025.25	03/04/2003	D745	A17	24	84	<b>13%</b>	<b>17%</b>	0%	<b>70%</b>
1ACER025.25	04/15/2003	D974	A17	14	27	<b>36%</b>	0%	<b>28%</b>	<b>36%</b>
1ACER025.25	05/12/2003	D1100	A17	24	260	<b>30%</b>	4%	<b>33%</b>	<b>33%</b>
1ACER025.25	06/25/2003	D1394	A17	24	140	<b>50%</b>	<b>25%</b>	<b>17%</b>	8%
1ACER025.25	07/22/2003	D1617	A17	24	440	<b>25%</b>	9%	<b>33%</b>	<b>33%</b>
1ACER025.25	08/18/2003	D1818	A17	24	300	<b>38%</b>	4%	<b>45%</b>	<b>13%</b>

**BOLD** type indicates a statistically significant value.

**Table 5.20 Bacterial Source Tracking for Licking Run at Station 1ALIL001.43.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ALIL001.43	08/27/2002	D6	A17	24	170	<b>50%</b>	0%	<b>50%</b>	0%
1ALIL001.43	09/30/2002	D34	A17	14	25	<b>79%</b>	0%	<b>21%</b>	0%
1ALIL001.43	10/17/2002	D67	A17	24	50,000	<b>42%</b>	0%	<b>25%</b>	<b>33%</b>
1ALIL001.43	11/13/2002	D144	A17	24	350	<b>62%</b>	0%	<b>38%</b>	0%
1ALIL001.43	12/16/2002	D330	A17	24	360	8%	0%	<b>21%</b>	<b>71%</b>
1ALIL001.43	01/29/2003	D570	A17	0	<1	--	--	--	--
1ALIL001.43	02/25/2003	D725	A17	16	67	13%	13%	<b>49%</b>	<b>25%</b>
1ALIL001.43	03/04/2003	D747	A17	23	130	9%	4%	<b>17%</b>	<b>70%</b>
1ALIL001.43	04/15/2003	D976	A17	23	86	<b>30%</b>	0%	13%	<b>57%</b>
1ALIL001.43	05/12/2003	D1102	A17	24	410	8%	0%	<b>42%</b>	<b>50%</b>
1ALIL001.43	06/25/2003	D1396	A17	24	380	<b>38%</b>	8%	13%	<b>41%</b>
1ALIL001.43	07/22/2003	D1619	A17	24	94	<b>46%</b>	0%	<b>46%</b>	8%

**BOLD** type indicates a statistically significant value.

**Table 5.21 Bacterial Source Tracking for Licking Run at Station 1ALIL008.23.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ALIL008.23	12/16/2002	D329	A17	24	170	<b>29%</b>	8%	<b>29%</b>	<b>34%</b>
1ALIL008.23	02/25/2003	D724	A17	8	18	0%	26%	37%	37%
1ALIL008.23	03/04/2003	D746	A17	8	22	13%	62%	0%	25%
1ALIL008.23	04/15/2003	D975	A17	24	150	<b>25%</b>	4%	<b>46%</b>	<b>25%</b>
1ALIL008.23	05/12/2003	D1101	A17	24	200	<b>29%</b>	0%	13%	<b>58%</b>
1ALIL008.23	06/25/2003	D1395	A17	24	460	<b>55%</b>	<b>29%</b>	8%	8%
1ALIL008.23	07/22/2003	D1618	A17	24	620	<b>42%</b>	8%	<b>42%</b>	8%
1ALIL008.23	08/18/2003	D1819	A17	24	150	0%	0%	<b>25%</b>	<b>75%</b>

**BOLD** type indicates a statistically significant value.

Table 5.22 Bacterial Source Tracking for Limestone Branch at Station 1ALIM001.16.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1ALIM001.16	08/27/2002	D1	A03	24	220	<b>55%</b>	<b>29%</b>	8%	8%
1ALIM001.16	09/30/2002	D32	A03	24	580	<b>17%</b>	<b>83%</b>	0%	0%
1ALIM001.16	10/17/2002	D65	A03	24	1,100	<b>17%</b>	0%	<b>50%</b>	<b>33%</b>
1ALIM001.16	11/13/2002	D142	A03	11	110	<b>37%</b>	18%	<b>27%</b>	18%
1ALIM001.16	12/16/2002	D325	A03	24	90	8%	0%	0%	<b>92%</b>
1ALIM001.16	01/29/2003	D569	A03	22	34	<b>59%</b>	<b>23%</b>	9%	9%
1ALIM001.16	02/25/2003	D722	A03	24	68	<b>29%</b>	8%	<b>25%</b>	<b>38%</b>
1ALIM001.16	03/04/2003	D744	A03	16	28	<b>38%</b>	6%	6%	<b>50%</b>
1ALIM001.16	04/15/2003	D973	A03	16	80	0%	<b>56%</b>	0%	<b>44%</b>
1ALIM001.16	05/12/2003	D1099	A03	24	260	0%	0%	0%	<b>100%</b>
1ALIM001.16	06/25/2003	D1393	A03	24	500	<b>38%</b>	4%	<b>20%</b>	<b>38%</b>
1ALIM001.16	07/22/2003	D1616	A03	24	510	<b>33%</b>	0%	<b>63%</b>	4%

**BOLD** type indicates a statistically significant value.

Table 5.23 Bacterial Source Tracking for Piney Run at Station 1APIA001.80.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1APIA001.80	08/27/2002	D3	A01	24	110	<b>54%</b>	0%	13%	<b>33%</b>
1APIA001.80	09/30/2002	D30	A01	24	200	<b>13%</b>	<b>13%</b>	<b>41%</b>	<b>33%</b>
1APIA001.80	10/17/2002	D63	A01	24	960	<b>21%</b>	0%	<b>46%</b>	<b>33%</b>
1APIA001.80	11/13/2002	D140	A01	22	190	<b>18%</b>	5%	<b>59%</b>	<b>18%</b>
1APIA001.80	12/16/2002	D327	A01	24	100	<b>29%</b>	0%	4%	<b>67%</b>
1APIA001.80	02/25/2003	D720	A01	24	64	<b>25%</b>	0%	<b>67%</b>	8%
1APIA001.80	03/04/2003	D742	A01	24	64	8%	0%	<b>50%</b>	<b>42%</b>
1APIA001.80	04/15/2003	D971	A01	24	90	<b>41%</b>	<b>21%</b>	<b>17%</b>	<b>21%</b>
1APIA001.80	05/12/2003	D1097	A01	24	120	<b>21%</b>	0%	<b>54%</b>	<b>25%</b>
1APIA001.80	06/25/2003	D1391	A01	24	120	<b>54%</b>	0%	0%	<b>46%</b>
1APIA001.80	07/22/2003	D1614	A01	24	460	<b>42%</b>	4%	<b>33%</b>	<b>21%</b>
1APIA001.80	08/18/2003	D1817	A01	24	410	<b>25%</b>	0%	<b>75%</b>	0%

**BOLD** type indicates a statistically significant value.



**Table 5.24 Bacterial Source Tracking for Unnamed Tributary to Limestone Branch at Station 1AXAQ000.85.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
1AXAQ000.85	08/27/2002	D2	A03	24	140	<b>29%</b>	<b>21%</b>	0%	<b>50%</b>
1AXAQ000.85	09/30/2002	D31	A03	24	370	4%	<b>25%</b>	<b>21%</b>	<b>50%</b>
1AXAQ000.85	10/17/2002	D64	A03	24	1,500	<b>21%</b>	0%	<b>38%</b>	<b>41%</b>
1AXAQ000.85	11/13/2002	D141	A03	24	890	<b>38%</b>	0%	<b>62%</b>	0%
1AXAQ000.85	12/16/2002	D326	A03	24	360	<b>42%</b>	0%	13%	<b>45%</b>
1AXAQ000.85	01/29/2003	D568	A03	23	56	<b>78%</b>	9%	0%	<b>13%</b>
1AXAQ000.85	02/25/2003	D721	A03	24	680	<b>13%</b>	0%	<b>79%</b>	8%
1AXAQ000.85	03/04/2003	D743	A03	24	60	<b>21%</b>	8%	<b>38%</b>	<b>33%</b>
1AXAQ000.85	04/15/2003	D972	A03	24	110	<b>21%</b>	8%	<b>46%</b>	<b>25%</b>
1AXAQ000.85	05/12/2003	D1098	A03	24	530	<b>17%</b>	0%	8%	<b>75%</b>
1AXAQ000.85	06/25/2003	D1392	A03	24	1,400	<b>50%</b>	<b>17%</b>	<b>25%</b>	8%
1AXAQ000.85	07/22/2003	D1615	A03	24	1,100	<b>33%</b>	8%	<b>38%</b>	<b>21%</b>

**BOLD** type indicates a statistically significant value.

**Table 5.25 Bacterial Source Tracking for Carter Run at Station 3CAE000.25.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3CAE000.25	12/17/2002	D380	E02	24	190	<b>25%</b>	<b>17%</b>	<b>50%</b>	8%
3CAE000.25	01/28/2003	D549	E02	16	22	<b>56%</b>	0%	<b>44%</b>	0%
3CAE000.25	03/05/2003	D757	E02	24	200	<b>46%</b>	8%	<b>42%</b>	4%
3CAE000.25	04/16/2003	D991	E02	24	200	<b>46%</b>	4%	4%	<b>46%</b>
3CAE000.25	05/20/2003	D1138	E02	24	310	<b>13%</b>	8%	<b>46%</b>	<b>33%</b>
3CAE000.25	06/23/2003	D1341	E02	24	290	<b>42%</b>	0%	<b>25%</b>	<b>33%</b>
3CAE000.25	07/21/2003	D1581	E02	24	390	<b>25%</b>	4%	<b>25%</b>	<b>46%</b>
3CAE000.25	08/19/2003	D1829	E02	24	160	<b>54%</b>	0%	13%	<b>33%</b>

**BOLD** type indicates a statistically significant value.

**Table 5.26 Bacterial Source Tracking for Deep Run at Station 3DPR001.70.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3DPR001.70	12/17/2002	D384	E10	24	35	<b>25%</b>	<b>54%</b>	4%	<b>17%</b>
3DPR001.70	01/28/2003	D551	E10	8	15	49%	13%	0%	38%
3DPR001.70	03/05/2003	D761	E10	24	44	<b>13%</b>	<b>25%</b>	8%	<b>54%</b>
3DPR001.70	04/16/2003	D995	E10	24	250	<b>29%</b>	0%	<b>54%</b>	<b>17%</b>
3DPR001.70	05/20/2003	D1142	E10	24	160	<b>13%</b>	4%	<b>33%</b>	<b>50%</b>
3DPR001.70	06/23/2003	D1345	E10	24	210	<b>13%</b>	8%	<b>25%</b>	<b>54%</b>
3DPR001.70	07/21/2003	D1585	E10	24	400	<b>33%</b>	0%	13%	<b>54%</b>
3DPR001.70	08/19/2003	D1833	E10	24	720	<b>21%</b>	8%	<b>58%</b>	<b>13%</b>

**BOLD** type indicates a statistically significant value.

**Table 5.27 Bacterial Source Tracking for Great Run at Station 3GRT001.70.**

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3GRT001.70	12/17/2002	D381	E02	8	70	13%	0%	87%	0%
3GRT001.70	03/05/2003	D758	E02	24	60	<b>17%</b>	<b>25%</b>	<b>17%</b>	<b>41%</b>
3GRT001.70	04/16/2003	D992	E02	24	78	<b>33%</b>	0%	<b>29%</b>	<b>38%</b>
3GRT001.70	05/20/2003	D1139	E02	24	410	<b>20%</b>	4%	<b>38%</b>	<b>38%</b>
3GRT001.70	06/23/2003	D1342	E02	24	140	<b>25%</b>	8%	<b>25%</b>	<b>42%</b>
3GRT001.70	07/21/2003	D1582	E02	24	230	<b>33%</b>	4%	13%	<b>50%</b>
3GRT001.70	08/19/2003	D1830	E02	24	170	<b>38%</b>	0%	13%	<b>49%</b>

**BOLD** type indicates a statistically significant value.

Table 5.28 Bacterial Source Tracking for Muddy Run at Station 3MUU000.82.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3MUU000.82	12/17/2002	D382	E07	24	100	8%	<b>25%</b>	<b>46%</b>	<b>21%</b>
3MUU000.82	03/05/2003	D759	E07	24	120	<b>33%</b>	<b>17%</b>	<b>29%</b>	<b>21%</b>
3MUU000.82	04/16/2003	D993	E07	24	260	<b>54%</b>	4%	13%	<b>29%</b>
3MUU000.82	05/20/2003	D1140	E07	24	680	4%	8%	<b>75%</b>	<b>13%</b>
3MUU000.82	06/23/2003	D1343	E07	24	240	<b>13%</b>	0%	<b>49%</b>	<b>38%</b>
3MUU000.82	07/21/2003	D1583	E07	24	310	<b>42%</b>	4%	<b>21%</b>	<b>33%</b>
3MUU000.82	08/19/2003	D1831	E07	24	100	<b>67%</b>	0%	<b>29%</b>	4%

**BOLD** type indicates a statistically significant value.

Table 5.29 Bacterial Source Tracking for Muddy Run at Station 3MUU008.52.

VADEQ ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	<i>E. coli</i> (cfu/100 ml)	Wildlife	Human	Livestock	Pet
3MUU008.52	12/17/2002	D383	E07	24	150	<b>21%</b>	<b>33%</b>	<b>17%</b>	<b>29%</b>
3MUU008.52	01/28/2003	D550	E07	8	12	100%	0%	0%	0%
3MUU008.52	03/05/2003	D760	E07	24	60	<b>21%</b>	<b>17%</b>	13%	<b>49%</b>
3MUU008.52	04/16/2003	D994	E07	24	700	4%	0%	<b>25%</b>	<b>71%</b>
3MUU008.52	05/20/2003	D1141	E07	23	1,700	4%	9%	<b>78%</b>	9%
3MUU008.52	06/23/2003	D1344	E07	24	610	8%	<b>13%</b>	<b>25%</b>	<b>54%</b>
3MUU008.52	07/21/2003	D1584	E07	24	1,800	<b>21%</b>	0%	<b>41%</b>	<b>38%</b>
3MUU008.52	08/19/2003	D1832	E07	24	1,500	<b>54%</b>	0%	<b>38%</b>	8%

**BOLD** type indicates a statistically significant value.

## **6. DISCUSSION**

Results of the first year of this study have been presented in this report. The ARCCs achieved during the library development stage are acceptable and there does not appear to be a high level of over-fitting. Based on the sample size targeted in each sample (*i.e.*, 24 isolates), there is 90% confidence that the proportions measured in each sample are within 15% of the actual proportions in the sampled population (*i.e.*, all bacteria in the stream at the time of sampling). Because a fixed-frequency sampling scheme was used, samples are not biased toward a particular flow regime and can therefore be combined to estimate the actual proportions contributed by the different sources over the entire year with greater precision (*i.e.*, 90% confidence that the estimate is within 5% of the actual proportions). Additionally, the statistical analyses applied to determine a significant difference from zero give a good indication of presence and absence of each source in each sample. All of these data are valuable for use in improving public awareness of the problem, improving model calibration/validation, and providing a more equitable allocation of loads to source classes.

In spite of the high quality of the data collected, care should be taken in using these data. These data represent, at most, 12 instantaneous observations at each station and may not be representative of long-term conditions. The hydrologic conditions during this period were extreme, beginning with drought and ending with some of the wettest seasons on record. Additionally, the dynamics of the bacterial community are not well understood, so care should be taken in extrapolating from the in-stream condition to activities in the watershed. As with any other monitoring program, the data should not be viewed in a vacuum. Local knowledge of the sources involved, historical water quality records, and the hydrologic conditions during sampling should all be considered in any interpretation of this data.

## REFERENCES

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## **Appendix C – Fecal Coliform Loads for Existing Conditions**

**Table C.1. Annual fecal coliform load to each land use by each source in the Deep Run Watershed.**

<b>Source</b>	<b>Crop (cfu/year)</b>	<b>Pasture-1 (cfu/year)</b>	<b>Pasture-2 (cfu/year)</b>	<b>Pasture-3 (cfu/year)</b>	<b>Urban (cfu/year)</b>	<b>Residential (cfu/year)</b>	<b>Loafing Lot (cfu/year)</b>	<b>Forest (cfu/year)</b>
<b><i>Human and Pets</i></b>								
Pets	0.0E+00	0.0E+00	0.0E+00	0.0E+00	8.1E+13	2.4E+14	0.0E+00	0.0E+00
Failed Septic Systems	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	3.6E+14	0.0E+00	0.0E+00
<b>Subtotal</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>8.1E+13</b>	<b>6.1E+14</b>	<b>0.0E+00</b>	<b>0.0E+00</b>
<b><i>Livestock</i></b>								
Dairy Cattle	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Beef Cattle	0.0E+00	3.1E+15	7.8E+14	1.9E+14	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Horses	0.0E+00	2.5E+13	1.3E+13	6.3E+12	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Sheep	0.0E+00	2.3E+14	1.5E+14	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Goats	0.0E+00	2.6E+14	1.7E+14	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
<b>Subtotal</b>	<b>0.0E+00</b>	<b>3.6E+15</b>	<b>1.1E+15</b>	<b>2.0E+14</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>
<b><i>Wildlife</i></b>								
Deer	1.5E+13	1.4E+13	7.2E+12	3.6E+12	0.0E+00	0.0E+00	0.0E+00	1.5E+14
Raccoons	1.6E+12	1.5E+12	7.6E+11	3.8E+11	0.0E+00	0.0E+00	0.0E+00	1.6E+13
Muskrats	2.7E+12	2.6E+12	1.3E+12	6.6E+11	0.0E+00	0.0E+00	0.0E+00	2.7E+13
Beavers	1.7E+08	1.6E+08	8.1E+07	4.1E+07	0.0E+00	0.0E+00	0.0E+00	1.7E+09
Geese	4.0E+13	3.9E+13	2.0E+13	9.8E+12	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Wild Turkeys	4.6E+11	4.4E+11	2.2E+11	1.1E+11	0.0E+00	0.0E+00	0.0E+00	4.5E+12
Ducks	2.9E+13	2.8E+13	1.4E+13	6.9E+12	0.0E+00	0.0E+00	0.0E+00	0.0E+00
<b>Subtotal</b>	<b>8.9E+13</b>	<b>8.6E+13</b>	<b>4.3E+13</b>	<b>2.1E+13</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>1.9E+14</b>
<b><i>Imported</i></b>								
Biosolids	1.0E+12	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
Poultry Litter	8.8E+11	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
<b>Subtotal</b>	<b>1.9E+12</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>	<b>0.0E+00</b>

**Table C.2. Monthly fecal coliform load directly deposited to each stream reach by each source in the Deep Run Watershed.**

Reach	Source	January (cfu/month)	February (cfu/month)	March (cfu/month)	April (cfu/month)	May (cfu/month)	June (cfu/month)
<b>D-1</b>	Livestock	8.6E+09	7.8E+09	1.3E+10	1.7E+10	2.6E+10	5.8E+10
	Wildlife	1.2E+12	1.1E+12	6.9E+11	6.7E+11	6.9E+11	6.7E+11
	Human	1.7E+11	1.6E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-2</b>	Livestock	4.3E+09	3.9E+09	6.4E+09	8.2E+09	1.3E+10	2.9E+10
	Wildlife	9.3E+11	8.5E+11	5.4E+11	5.2E+11	5.4E+11	5.2E+11
	Human	1.7E+11	1.6E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-3</b>	Livestock	8.8E+09	8.0E+09	1.3E+10	1.7E+10	2.6E+10	5.9E+10
	Wildlife	1.1E+12	1.0E+12	6.3E+11	6.1E+11	6.3E+11	6.1E+11
	Human	3.5E+11	3.2E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11
<b>D-4</b>	Livestock	2.8E+09	2.6E+09	4.3E+09	5.5E+09	8.5E+09	1.9E+10
	Wildlife	1.0E+12	9.5E+11	6.0E+11	5.8E+11	6.0E+11	5.8E+11
	Human	1.7E+11	1.6E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-5</b>	Livestock	4.8E+09	4.4E+09	7.2E+09	9.3E+09	1.4E+10	3.2E+10
	Wildlife	1.2E+12	1.1E+12	6.6E+11	6.3E+11	6.6E+11	6.3E+11
	Human	3.5E+11	3.2E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11
<b>D-6</b>	Livestock	5.1E+09	4.7E+09	7.7E+09	9.9E+09	1.5E+10	3.5E+10
	Wildlife	1.1E+12	9.8E+11	6.2E+11	6.0E+11	6.2E+11	6.0E+11
	Human	1.7E+11	1.6E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-7</b>	Livestock	1.8E+10	1.6E+10	2.7E+10	3.4E+10	5.3E+10	1.2E+11
	Wildlife	1.4E+12	1.3E+12	8.5E+11	8.2E+11	8.5E+11	8.2E+11
	Human	3.5E+11	3.2E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11
<b>D-8</b>	Livestock	5.4E+08	4.9E+08	8.1E+08	1.0E+09	1.6E+09	3.6E+09
	Wildlife	3.8E+11	3.4E+11	2.2E+11	2.1E+11	2.2E+11	2.1E+11
	Human	1.7E+11	1.6E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11



**Table C.2. (cont'd) Monthly fecal coliform load directly deposited to each stream reach by each source in the Deep Run Watershed.**

Reach	Source	July (cfu/month)	August (cfu/month)	September (cfu/month)	October (cfu/month)	November (cfu/month)	December (cfu/month)
<b>D-1</b>	Livestock	6.0E+10	6.0E+10	2.5E+10	1.7E+10	1.2E+10	8.6E+09
	Wildlife	6.9E+11	6.9E+11	1.2E+12	1.2E+12	1.2E+12	1.2E+12
	Human	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-2</b>	Livestock	3.0E+10	3.0E+10	1.2E+10	8.5E+09	6.2E+09	4.3E+09
	Wildlife	5.4E+11	5.4E+11	9.0E+11	9.3E+11	9.0E+11	9.3E+11
	Human	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-3</b>	Livestock	6.1E+10	6.1E+10	2.5E+10	1.8E+10	1.3E+10	8.8E+09
	Wildlife	6.3E+11	6.3E+11	1.1E+12	1.1E+12	1.1E+12	1.1E+12
	Human	3.5E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11	3.5E+11
<b>D-4</b>	Livestock	2.0E+10	2.0E+10	8.2E+09	5.7E+09	4.1E+09	2.8E+09
	Wildlife	6.0E+11	6.0E+11	1.0E+12	1.0E+12	1.0E+12	1.0E+12
	Human	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-5</b>	Livestock	3.4E+10	3.4E+10	1.4E+10	9.6E+09	7.0E+09	4.8E+09
	Wildlife	6.6E+11	6.6E+11	1.2E+12	1.2E+12	1.2E+12	1.2E+12
	Human	3.5E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11	3.5E+11
<b>D-6</b>	Livestock	3.6E+10	3.6E+10	1.5E+10	1.0E+10	7.4E+09	5.1E+09
	Wildlife	6.2E+11	6.2E+11	1.0E+12	1.1E+12	1.0E+12	1.1E+12
	Human	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11
<b>D-7</b>	Livestock	1.2E+11	1.2E+11	5.1E+10	3.5E+10	2.6E+10	1.8E+10
	Wildlife	8.5E+11	8.5E+11	1.4E+12	1.4E+12	1.4E+12	1.4E+12
	Human	3.5E+11	3.5E+11	3.4E+11	3.5E+11	3.4E+11	3.5E+11
<b>D-8</b>	Livestock	3.8E+09	3.8E+09	1.6E+09	1.1E+09	7.8E+08	5.4E+08
	Wildlife	2.2E+11	2.2E+11	3.6E+11	3.8E+11	3.6E+11	3.8E+11
	Human	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11	1.7E+11

**Table C.3. Daily fecal coliform load applied to each land use by month for subwatershed D-1 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
February	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
March	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
April	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
May	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
June	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
July	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
August	1.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
September	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
October	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
November	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07
December	2.0E+08	7.0E+09	5.0E+09	2.0E+09	3.0E+09	1.0E+10	4.0E+07

**Table C.4. Daily fecal coliform load applied to each land use by month for subwatershed D-2 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
February	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
March	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
April	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
May	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
June	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
July	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
August	2.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
September	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
October	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
November	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07
December	4.0E+08	9.0E+09	7.0E+09	2.0E+09	2.0E+10	7.0E+10	4.0E+07

**Table C.5. Daily fecal coliform load applied to each land use by month for subwatershed D-3 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
February	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
March	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
April	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
May	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
June	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
July	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
August	2.0E+08	8.0E+09	5.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
September	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
October	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
November	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07
December	3.0E+08	8.0E+09	6.0E+09	2.0E+09	7.0E+11	1.0E+10	4.0E+07

**Table C.6. Daily fecal coliform load applied to each land use by month for subwatershed D-4 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
February	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
March	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
April	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
May	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
June	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
July	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
August	1.0E+08	7.0E+09	4.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
September	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
October	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
November	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07
December	2.0E+08	7.0E+09	5.0E+09	2.0E+09	4.0E+11	1.0E+10	4.0E+07

**Table C.7. Daily fecal coliform load applied to each land use by month for subwatershed D-5 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07
February	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07
March	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
April	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
May	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
June	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
July	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
August	1.0E+08	3.0E+09	2.0E+09	9.0E+08	2.0E+10	9.0E+10	4.0E+07
September	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07
October	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07
November	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07
December	2.0E+08	4.0E+09	2.0E+09	1.0E+09	2.0E+10	9.0E+10	4.0E+07

**Table C.8. Daily fecal coliform load applied to each land use by month for subwatershed D-6 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07
February	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07
March	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
April	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
May	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
June	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
July	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
August	1.0E+08	4.0E+09	2.0E+09	9.0E+08	3.0E+11	4.0E+07
September	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07
October	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07
November	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07
December	3.0E+08	4.0E+09	3.0E+09	1.0E+09	3.0E+11	4.0E+07

**Table C.9. Daily fecal coliform load applied to each land use by month for subwatershed D-7 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Residential (cfu/ac-day)	Forest (cfu/ac-day)
January	2.0E+08	1.0E+10	6.0E+09	4.0E+09	1.0E+10	4.0E+10	4.0E+07
February	3.0E+08	1.0E+10	6.0E+09	4.0E+09	1.0E+10	4.0E+10	4.0E+07
March	8.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
April	7.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
May	2.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
June	1.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
July	1.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
August	1.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
September	2.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
October	3.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
November	4.0E+08	1.0E+10	7.0E+09	5.0E+09	1.0E+10	4.0E+10	4.0E+07
December	2.0E+08	1.0E+10	6.0E+09	4.0E+09	1.0E+10	4.0E+10	4.0E+07

**Table C.10. Daily fecal coliform load applied to each land use by month for subwatershed D-8 in the Deep Run watershed.**

Month	Crop (cfu/ac-day)	Pasture-1 (cfu/ac-day)	Pasture-2 (cfu/ac-day)	Pasture-3 (cfu/ac-day)	Commercial (cfu/ac-day)	Forest (cfu/ac-day)
January	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
February	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
March	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
April	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
May	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
June	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
July	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
August	2.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
September	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
October	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
November	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07
December	4.0E+08	7.0E+09	6.0E+09	1.0E+09	4.0E+10	4.0E+07